

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 14:29:37 ; Search time 12078 Seconds  
(without alignments)  
12967.970 Million cell updates/sec

Title: US-09-697-898-1

Perfect score: 5245

Sequence: 1 gagaaatggcggcgccgc.....tttcaaaccaaaaaaaaaa 5245

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rtd:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	843.4	16.1	893	13	BUI72741
2	787.8	15.0	836	9	AUI32367
3	738.8	14.1	895	13	BUI94120
4	682.4	13.0	1043	12	BM928438

CF409553	CH3#061_D	949	14	CF409553	11.5	601	5
AL042445	DXF2P434D	653	9	AL042445	11.4	598	6
BI654958	603283220	868	12	BI654958	11.1	583	7
CAS12935	UI-R-FU0-	799	14	CAS12935	10.4	546.8	8
AJ450706	AJ450706	716	9	AJ450706	10.4	544	9
AW499603	UI-HF-BP0	530	10	AW499603	9.9	519.8	10
CF143161	UI-HF-BR0	526	14	CF143161	9.9	518.8	11
CAS12956	UI-R-FU0-	752	14	CAS12956	9.8	514	12
BI655574	603284924	719	12	BI655574	9.6	504	13
CF287689	AGENCOURT	773	14	CF287689	9.5	500.8	14
BA485112	DKF2P686N	499	13	BA485112	9.5	497.4	15
BE162514	FML-HT045	642	10	BE162514	9.4	495.4	16
BB981914	UI-M-CG0P	714	10	BB981914	9.4	494.2	17
AW916314	EST347618	624	10	AW916314	9.3	485.6	18
CF519921	AGENCOURT	696	14	CF519921	9.2	484.6	19
BE981478	UI-M-CG0P	714	10	BE981478	9.2	484.2	20
BM148300	TCAAP121	486	12	BM148300	9.1	479.6	21
AJ442678	AJ442678	768	9	AJ442678	9.1	476.4	22
AI538525	td07g08.X	473	9	AI538525	9.0	473	23
AX095560	DX095560	472	13	AX095560	9.0	472	24
AL135609	DKF2P762F	470	9	AL135609	9.0	470	25
AW502619	UI-HF-BR0	476	10	AW502619	9.0	470	26
CB559647	AGENCOURT	830	14	CB559647	8.7	458.4	27
BUI12915	603131085	870	13	BUI12915	8.7	457.6	28
BE242824	TCAAP1821	460	10	BE242824	8.7	455.2	29
CF409554	CH3#061_D	834	14	CF409554	8.6	451.2	30
BU904431	AGENCOURT	881	13	BU904431	8.5	448.2	31
AI684800	wa73g11.X	452	9	AI684800	8.5	445.6	32
BQ830084	LL6in2176	592	13	BQ830084	8.4	443.4	33
AW580454	BM1-HT045	492	10	AW580454	8.4	439.8	34
BF465762	UI-M-CG0P	511	10	BF465762	8.3	434.8	35
BE956678	UI-M-BG2-	595	10	BE956678	8.2	431.8	36
CF143770	UI-HF-BP0	431	14	CF143770	7.8	411.2	37
AW501166	UI-HF-BP0	420	10	AW501166	7.8	408.8	38
BQ430775	AGENCOURT	903	13	BQ430775	7.7	403.4	39
BE853080	uw29c02.X	556	10	BE853080	7.6	397.2	40
CG672158	RRI183_Ba	502	29	CG672158	7.4	386.8	41
BF086951	RC3-HT023	405	10	BF086951	7.3	385.4	42
BI343321	371394_MA	456	12	BI343321	7.3	381	43
BF466352	UI-M-CG0P	552	10	BF466352	7.2	380	44
BY748459	BY748459	670	13	BY748459	7.2	379.4	45

#### ALIGNMENTS

RESULT 1  
BUI72741  
LOCUS BUI72741 893 bp mRNA linear EST 04-SEP-2002  
DEFINITION AGENCOURT 7964791 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6169242  
5' RNA sequence:  
ACCESSION BUI72741  
VERSION BUI72741  
KEYWORDS EST.  
SOURCE BUI72741.1 GI:226866725  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 893)  
NIH-MGC <http://mgc.nci.nih.gov/>  
National Institutes of Health  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DTF  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1AM13534 row: a column: 19  
High quality sequence stop: 671.



4311	QY	TGCGCTGCTATTTATAGAAATGGCTTGTGCAGAAACCAACATGGAATGCGAGAAAAACACTC	4370
301	Db	TGCGCTGCTATTTATAGAAATGGCTTGTGCAGAAACCAACATGGAATGCGAGAAAAACACTC	360
4371	QY	CAATCACTTTGCTTTTCATATTTAAGATTGCTAGTGCAACTACTGCTCCCACTCGATCCCTTC	4430
361	Db	CAATCACTTTGCTTTTGTATTTAANATTGCTAGTGCAACTACTGCTCCATCGATCCCTTC	420
4431	QY	ACATTTGCTCCCGGTTTACGAGATGCGGCTCTTTGGTTGTTAGAACTTCAACCTCAGGA	4490
421	Db	ACATTTGCTCCCGGTTTACGAGATGCGGCTCTTTGGTTGTTAGAACTTCAACCTCAGGA	480
4491	QY	CAGACCTCCATCAAGAGAGCTACTGGAAGCATCCAGTCTTTCGTACTACATGGTAGCCAAT	4550
481	Db	CAGACCTCCATCAANAGAGCTACTGGAAGCATCCAGTCTTTCGTACTACATGGTAGCCAAT	540
4551	QY	TATGCAGATCAACTACAGTAGAAACAGATGCTCAACAAGAGAAAAAAACCTTTGTGGGA	4610
541	Db	TATGCAGATCAACTACAGTAGAAACAGATGCTCAACAAGAGAAAAAAACCTTTGTGGGA	600
4611	QY	ACCACATTCGATTTCTACTTGGCCATGATGCCACTGAACAGCTATGAACAGGGCCAGTGGG	4670
601	Db	ACCACATTCGATTTCTACTTGGCCATGATGCCACTGAACAGCTATGAACAGGGCCAGTGGG	660
4671	QY	GAACCCCTTACCTAAGTATGTGATGTAACAATCATGATCTGTAACCTAAGCTCAGTAGCAA	4730
661	Db	GAACCCCTTACCTAAGTATGTGATGTAACAATCATGATCTGT-CCTAAGCTCAGTAGCAA	719
4731	QY	AGGCCCAAACTAGTCGAGAAACGTAAACTGTGCCCTTCAAAGCACTGGGCCCTTAGGTGA	4790
720	Db	AGGCCCAAACTAGTCGAG-AACTGTAAACTGTGCCCTTCAAAGCACTGGGCCCTTAGGTGA	778
4791	QY	CAGGAAACAACTGAAGTTTGCATGACTAAATTGCAAGACATAATTTATTTTTTGA	4849
779	Db	CAGG-AAACCACTGAATTTTCATGACTAAATTCGAGAAACCTTAATTTATTTTTTGA	836

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RESULT 3
BU194120
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BU194120      895 bp      mRNA      linear      EST 04-SEP-2002
AGENCOURT_7968818 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6148258
5', mRNA sequence.
BU194120      BU194120      1      GI-22708104
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 895)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DMP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: L1M13479 row: g column: 11
High quality sequence stop: 568.
Location/Qualifiers
1..895
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6148258"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"

FEATURES
source

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FEATURES  
SOURCE

ORIGIN			
Query Match	14.1%; Score 738.8; DB 13; Length 895;		
Best Local Similarity	98.5%; Pred. No. 2.6e-118;		
Matches 767; Conservative	0; Mismatches 8; Indels 4; Gaps 2;		
QY	3599	CTCAGGATCCCTCCCCATAGTTTCTCAGCTGCAGGTTGAAATGGAGAGATATCATCA	3658
Db	53	CGCAGGATCCCTCCCCATAGTTTCTCAGCTGCAGGTTGAAATGGAGAGATATCATCA	112
QY	3659	TTATTCAACAGGATACACAGAGACTCTACCAGGACATACCACAAACACACCGTATA	3718
Db	113	TTATTCAACAGGATACACAGAGACTCTACCAGGACATACCACAAACACACCGTATA	172
QY	3719	GAGAAGACACTGAATGGCTGAAAGGTCAACAGATAGGCCCTTGAGAGATTTCTTCTTGTT	3778
Db	173	GAGAAGACACTGAATGGCTGAAAGGTCAACAGATAGGCCCTTGAGAGATTTCTTCTTGTT	232
QY	3779	ATCAGGCTCAAGATGTGGGAACCTGGAACCTTTAATGGCTGTTTAAACAGGTGACTTATGTCA	3838
Db	233	ATCAGGCTCAAGATGTGGGAACCTGGAACCTTTAATGGCTGTTTAAACAGGTGACTTATGTCA	292
QY	3839	GAAACACATCTTCTGAGCAAGAGAAAGTAGTAGAAGCACCTAAGAGAGAGATAGAAATGA	3898
Db	293	GAAACACATCTTCTGAGCAAGAGAAAGTAGTAGAAGCACCTAAGAGAGAGATAGAAATGA	352
QY	3899	TGAGCCATCTGAATCATCAAAACATCATTAGGATGTGGAGCCACGTTGAGAGAGCA	3958
Db	353	TGAGCCATCTGAATCATCAAAACATCATTAGGATGTGGAGCCACGTTGAGAGAGCA	412
QY	3959	ATTACAACTCTTCATTGATGATGCGAGCGGGGGATCGGTGGCTCATTTCTCTGAGTAAAT	4018
Db	413	ATTACAACTCTTCATTGATGATGCGAGCGGGGGATCGGTGGCTCATTTCTCTGAGTAAAT	472
QY	4019	ATGGAGCCCTTCAAAGAAATCAGTAGTTTATTAACCTACACTGAAACAGTTACTCCGTGGCCCTTT	4078
Db	473	ATGGAGCCCTTCAAAGAAATCAGTAGTTTATTAACCTACACTGAAACAGTTACTCCGTGGCCCTTT	532
QY	4079	CGTATCTCCATGAAACCAAATCATTCACAGAGATGTCAAAAGTGGCAATTTGCTAATTG	4138
Db	533	CGTATCTCCATGAAACCAAATCATTCACAGAGATGTCAAAAGTGGCAATTTGCTAATTG	592
QY	4139	ACAGCACTGGTCCAGAGACTAAGAAATTCAGATTTTGGAGCTGCAGCCAGGTTGGCATCAA	4198
Db	593	ACAGCACTGGTCCAGAGACTAAGAAATTCAGATTTTGGAGCTGCAGCCAGGTTGGCATCAA	652
QY	4199	AAGGAACCTGGTCAGGAGAGTTTCAGGGAACAATTACTGGGGAACAATTGCATTTATGGCAC	4258
Db	653	AAGGAACCTGGTCAGGAGAGTTTCAGGGAACAATTACTGGGGAACAATTGCATTTATGGCAC	712
QY	4259	CTGAGGTACTTAACAGGTCAACAGTATGGAAGGAGCTGTGATGTATGAGTGGTT--GGCTGT	4317
Db	713	CTGAGGTACTTAACAGGTCAACAGTATGGAAGGAGCTGTGATGTATGAGTGGTTGGGCTGT	772
QY	4318	GCTATTATAGAAATGCTTTGTGCAAAACCCACC---ATGGAATCGAGAAAAACACTCCAA	4373
Db	773	GCTATTATAGAAATGCTTTGTGCAAAACCCACCATGGGNAATCGAGAAAAACACTCCCA	831
RESULT 4			
BM928438			
LOCUS	1043 bp mRNA linear EST 12-MAR-2002		
DEFINITION	AGENCOURT_6699830 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770238		
ACCESSION	5', mRNA sequence.		
VERSION	BM928438		
KEYWORDS	BM928438.1 GI:19378817		
SOURCE	Est.		
ORGANISM	Homo sapiens (human)		
	Homo sapiens		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)

Tissue procurement: Life Technologies, Inc.

cDNA library preparation: Life Technologies, Inc.

cDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12832 row: p column: 15

High quality sequence stop: 625.

Location/Qualifiers

1..1043

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5770238"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_121"

/note="Organ: Brain; Vector: pCMV-Sport6; Site\_1: NotI;

Site\_2: EcoRV (destroyed); RNA source anonymous pool of 3

fetal brains, female age 20 weeks, female age 24 weeks,

and male age 26 weeks. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range

0.7-3.5 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 017. Note:

this is a NIH\_MGC Library."

#### ORIGIN

Query Match 13.0%; Score 682.4; DB 12; Length 1043;

Best Local Similarity 99.0%; Pred. No. 1.8e-108;

Matches 697; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 4541 GGTAGCAATTATGACATCACTACAGTAGAAGAGGATGCTCAACAGAGAAAAAAA 4600

DB 1 GGTAGCAATTATGACATCACTACAGTAGAAGAGGATGCTCAACAGAGAAAAAAA 60

QY 4601 CTT-GTGGGGAACCACTATGATTTCTACTGGCCATGATGCCACTGAACAGCTATGAACG 4659

DB 61 CTTGGTGGGAACCACTATGATTTCTACTGGCCATGATGCCACTGAACAGCTATGAACG 120

QY 4660 AGCCAGTGGGAACCCCTTACCTAAGTATGTGATGACAAATCATGATCTGACCTAAGC 4719

DB 121 AGCCAGTGGGAACCCCTTACCTAAGTATGTGATGACAAATCATGATCTGACCTAAGC 180

QY 4720 TCAGTATGCAAAAGCCCAACTAGTCAGAACTGTAACTGTGCTTTCAAGAACTGG 4779

DB 181 TCAGTATGCAAAAGCCCAACTAGTCAGAACTGTAACTGTGCTTTCAAGAACTGG 240

QY 4780 CCTAGTGCAACAGGAAAAACAATGAAGTTGGCATGCTAAATTCGACAGCAATATTTA 4839

DB 241 CCTAGTGCAACAGGAAAAACAATGAAGTTGGCATGCTAAATTCGACAGCAATATTTA 300

QY 4840 TTTTGGAGCACTTTTCAGCAATATTAGCGGCTGAGGGCTCAGGATCTATTTAAT 4899

DB 301 TTTTGGAGCACTTTTCAGCAATATTAGCGGCTGAGGGCTCAGGATCTATTTAAT 360

QY 4900 ATTTCAATATTTCTCCATTTATATAGTATGATCAACAGCAGGGGTTCTGCAATTCGGT 4959

DB 361 ATTTCAATATTTCTCCATTTATATAGTATGATCAACAGCAGGGGTTCTGCAATTCGGT 420

QY 4960 CAAATTTTGTCACTGGCTATAAATCAGTATCTGCCTCTTTTAGGTCAAGTAGTCTA 5019

DB 421 CAAATTTTGTCACTGGCTATAAATCAGTATCTGCCTCTTTTAGGTCAAGTAGTCTA 480

QY 5020 TGAGTAGCAATACATACATATATTTTAAAGTGTGATCTTTTATGACCCACAGTTGA 5079

DB 481 TGAGTAGCAATACATACATATATTTTAAAGTGTGATCTTTTATGACCCACAGTTGA 540

QY 5080 CCTTATTTTCTTAATACCAGGAGTGGCTCATGTCATTGCTTACTCTTGGCCCA 5139

DB 541 CCTTATTTTCTTAATACCAGGAGTGGCTCATGTCATTGCTTACTCTTGGCCCA 600

QY 5140 TTCAATTCGTTTTTGGAAATATGTTTTGATTTTCAATTTTATTTATCAATTCATTTTG 5199

DB 601 TTCAATTCGTTTTTGGAAATATGTTTTGATTTTCAATTTTATTTATCAATTCATTTTG 660

QY 5200 TTATTCAGGAAAGCTGATCTTTTTCACACCAAAAAA 5243

DB 661 TTATTCAGGAAAGCTGATCTTTTTCACACCAAAAAA 704

#### FEATURES

source

CF409553 949 bp mRNA linear EST 02-SEP-2003

CH3#061\_D05MF Canine heart normalized cDNA Library in pBluescript

Canis familiaris cDNA clone CH3#061\_D05 5', mRNA sequence.

CF409553

CF409553.1 GI:34410799

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 949)

Expressed sequence tags from Canine heart

Unpublished (2003)

Other ESTs: CH3#061\_D05ME

Contact: George AL

Division of Genetic Medicine

Vanderbilt University

529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA

Tel: 615 936 2660

Fax: 615 936 2661

Email: [al.george@vanderbilt.edu](mailto:al.george@vanderbilt.edu)

Insert Length: 1552 Std Error: 0.00

Seq primer: MF: GTTTCCTCCAGTCACGACGTTG

High quality sequence start: 165

High quality sequence stop: 780.

Location/Qualifiers

1..949

/organism="Canis familiaris"

/mol\_type="mRNA"

/db\_xref="taxon:9615"

/clone="CH3#061\_D05"

/tissue\_type="heart"

/cell\_type="heart"

/dev stage="mixed developmental stages (adult, 30 day - 40

day fetal)"

/clone\_lib="Canine heart normalized cDNA Library in

pBluescript"

/note="Organ: heart; Vector: pBluescript; Site\_1: 5' of

vector NotI; Site\_2: 3' of vector EcoRI; Tissue source:

dog heart (adult, 30 day - 40 day fetal), right and left

atria and ventricle. Dog breed - mixed (beagle, German

shepherd, pointer, Irish setter). Library construction:

oligo-dT primed"

Query Match 11.5%; Score 601; DB 14; Length 949;

Best Local Similarity 92.6%; Pred. No. 2.7e-94;

Matches 653; Conservative 0; Mismatches 50; Indels 2; Gaps 2;

QY 4069 CGTGGCTTTTCGATCTCCATGAAACCAATCATTCACAGAGATGCAAGGTGCCAAT 4128

DB 165 CGTGGCTTTTCGATCTCCATGAAACCAATCATTCATAGATGTCAAAGGTGCCAAT 224



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QY 4129 TTGCTAAATTGACAGCACTGGTCAGAGACTAAGAAATTGAGATTTTGGAGCTGCAGCCAGG 4188
Db 225 TTGCTAAATTGACAGCACAGGTCAGAGACTGAGAAATTGAGATTTTGGAGCTGCAGCCAGG 284
QY 4189 TTGGCATCAAAAGGAACCTGGTCAGGAGAGTTTCAGGACAAATTACTTGGGACAAATTGCA 4248
Db 285 TTGGCATCAAAAGGAACCTGGTCAGGAGAGTTTCAGGACAAATTACTTGGGACAAATTGCA 344
QY 4249 TTTATGGCACCTGAGGTACTAAGAGGTCACAGTAGTATGGAAGGAGCTGTGATGTATGGAGT 4308
Db 345 TTTATGGCACCTGAGGTACTGAGAGTCAGAGTAGTATGGAAGGAGCTGTGATGTATGGAGT 404
QY 4309 GTTGGCTGTGCTATATAGAAATGCTTGTGCAAAACCAACCATGAGTATGCAAAACAC 4368
Db 405 GTTGGCTGTGCTATATAGAAATGCTTGTGCAAAACCAACCATGAGTATGCAAAACAC 464
QY 4369 TCCATATCATCTGCTTTGATATTTAAGATTTGATGCTCAACTACTGCTCCCATGATCCCT 4428
Db 465 TCCATATCATCTGCTTTGATATTTAAGATTTGCAAGTGGAGGACTGCTCCCATGATCCCT 524
QY 4429 TCACATTTGCTCCCTGGTTTACGAGATGTGGCTCTTCTGTTTGTAGAACTTCAACCTCAG 4488
Db 525 TCACATTTGCTCCCTGGTTTACGAGATGTGGCTCTTCTGTTTGTAGAACTTCAACCTCAG 584
QY 4489 GACAGACCTCCATCAAGAGAGCTACTGAAGCATCCAGTCTTTCTGCTACTACATGCTAGCA 4548
Db 585 GACAGACCTCCATCAAGAGAGCTACTGAAGCATCCAGTCTTTCTGCTACTACATGCTAGCA 644
QY 4549 ATTATGCAAGTCAACTACAGTAGTAAAGAGGATGCTCAACAGAGAAAAAACTTTGGG 4608
Db 645 ATTATGCAAGTCAACTACAGTAGTAAAGAGGATGCTCAACAGAG-CAAAACTTTTGTGGG 703
QY 4609 GAACACATTTGATTTCTACTGGCCATGATGCTGCAAGTATGCAAGGAGGAGGAGG 4668
Db 704 GAACACATTTGATTTCTACTGGCCATGATGCTGCAAGTATGCAAGGAGGAGGAGGAGG 763
QY 4669 GGGAAACCTTCACTAAGTATGTGATGCAAAATCATGATCTGTACTAAGCTCAGTAGTC 4728
Db 764 GGGAAACCTTCACTAAGTATGTGATGCAAAATCATGATCTGTACTAAGCTCAGTAGTC 823
QY 4729 AAAAGCCCA-ACCTAGTGCAGAACTGTAAACTGTGCTTCAAA 4772
Db 824 AAAAGTCCCAATTTGTGCAGAACTGTAAACTGTGCTTCAAA 868

RESULT 6
AL042445 653 bp mRNA linear EST 04-SEP-2003
LOCUS DKFp434D2221_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DEFINITION DKFp434D2221 5', mRNA sequence.
ACCESSION AL042445
VERSION AL042445.1 GI:5421814
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
AUTHORS This is the 5' sequence of the clone insert
TITLE Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
JOURNAL Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de;
COMMENT sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No 5' sequence available.
This clone (DKFp434D2221) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
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FEATURES
source
1..653
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFp434D2221"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match 11.4%; Score 598; DB 9; Length 653;
Best Local Similarity 98.6%; Pred. NO. 8.8e-94;
Matches 624; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

QY 3856 CAGAGAGAGTAGTAAAGCACTAGAGAGAGAGATAGATGATGAGCCATCTGAATCAT 3915
Db 1 CAAGAAGAGAGTAGTAAAGCACTAGAGAGAGAGATAGATGATGAGCCATCTGAATCAT 60
QY 3916 CCAAAACATCATTAGGATGTTGGAGCCACGTGTGAGAGAGCAATPACAATCTCTTCATT 3975
Db 61 CCAAAACATCATTAGGATGTTGGAGCCACGTGTGAGAGAGCAATPACAATCTCTTCATT 120
QY 3976 GAATGATGCGAGGGGATGCGTGGCTCATTTGCTGAGTAAATATGAGCCCTTCAAGAA 4035
Db 121 GAATGATGCGAGGGGATGCGTGGCTCATTTGCTGAGTAAATATGAGCCCTTCAAGAA 180
QY 4036 TCAGTAGTATTATTAACTACACTGAACAGTACTACCTGGGCTTTTCGTATCTCCATGAAAAC 4095
Db 181 TCAGTAGTATTATTAACTACACTGAACAGTACTACCTGGGCTTTTCGTATCTCCATGAAAAC 240
QY 4096 CAAATCATTCACAGAGATGTCAAAGGTGCCAATTTGCTTAATTGACAGACTGTGTCAGAGA 4155
Db 241 CAAATCATTCACAGAGATGTCAAAGGTGCCAATTTGCTTAATTGACAGACTGTGTCAGAGA 300
QY 4156 CTAAGAATTCAGATTTTGGAGCTGCAGCCAGGTTGGCATCAAAGGAACTGGTGCAGGA 4215
Db 301 CTAAGAATTCAGATTTTGGAGCTGCAGCCAGGTTGGCATCAAAGGAACTGGTGCAGGA 360
QY 4216 GAGTTTCAGGACAAATTACTTGGGACAAATTGCAATTTATGGCACCTGAGGTACTAAGAGGT 4275
Db 361 GAGTTTCAGGACAAATTACTTGGGACAAATTGCAATTTATGGCACCTGAGGTACTAAGAGGT 420
QY 4276 CAACAGTATGGAAGGAGCTGTGATGATGAGTGTGGCTGTGCTATTATAGAAATGGCT 4335
Db 421 CAACAGTATGGAAGGAGCTGTGATGATGAGTGTGGCTGTGCTATTATAGAAATGGCT 480
QY 4336 TGTGCAAAACCCACCATGGAATGCAGAAAAACACTCCAATCATCTTCTTTGATATTAAAG 4395
Db 481 TGTGCAAAACCCACCATGGAATGCAGAAAAACACTCCAATCATCTTCTTTGATATTAAAG 540
QY 4396 ATTGCTAGTGCACACTACTGCTCCATCGATCCCTTCACTTTGCTGCTGCTGTTTACGA --G 4453
Db 541 ATTGCTAGTGCACACTACTGCTCCATCGATCCCTTCACTTTGCTGCTGCTGTTTACGAAGA 600
QY 4454 ATGTGGCTCTTCTGTTGTTT-AGAATTTCAACCT 4485
Db 601 TGTGGCTCTTCTGTTGTTTAAAGAACTTCAACCT 633

RESULT 7
BI654958 868 bp mRNA linear EST 12-SEP-2001
LOCUS 603283220F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5327644 5',
DEFINITION mRNA sequence.
ACCESSION BI654958
VERSION BI654958.1 GI:15569194
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
```

```
QY 4129 TTGCTAAATTGACAGCACTGGTCAGAGACTAAGAAATTGAGATTTTGGAGCTGCAGCCAGG 4188
Db 225 TTGCTAAATTGACAGCACAGGTCAGAGACTGAGAAATTGAGATTTTGGAGCTGCAGCCAGG 284
QY 4189 TTGGCATCAAAAGGAACCTGGTCAGGAGAGTTTCAGGACAAATTACTTGGGACAAATTGCA 4248
Db 285 TTGGCATCAAAAGGAACCTGGTCAGGAGAGTTTCAGGACAAATTACTTGGGACAAATTGCA 344
QY 4249 TTTATGGCACCTGAGGTACTAAGAGGTCACAGTAGTATGGAAGGAGCTGTGATGTATGGAGT 4308
Db 345 TTTATGGCACCTGAGGTACTGAGAGTCAGAGTAGTATGGAAGGAGCTGTGATGTATGGAGT 404
QY 4309 GTTGGCTGTGCTATATAGAAATGCTTGTGCAAAACCAACCATGAGTATGCAAAACAC 4368
Db 405 GTTGGCTGTGCTATATAGAAATGCTTGTGCAAAACCAACCATGAGTATGCAAAACAC 464
QY 4369 TCCATATCATCTGCTTTGATATTTAAGATTTGATGCTCAACTACTGCTCCCATGATCCCT 4428
Db 465 TCCATATCATCTGCTTTGATATTTAAGATTTGCAAGTGGAGGACTGCTCCCATGATCCCT 524
QY 4429 TCACATTTGCTCCCTGGTTTACGAGATGTGGCTCTTCTGTTTGTAGAACTTCAACCTCAG 4488
Db 525 TCACATTTGCTCCCTGGTTTACGAGATGTGGCTCTTCTGTTTGTAGAACTTCAACCTCAG 584
QY 4489 GACAGACCTCCATCAAGAGAGCTACTGAAGCATCCAGTCTTTCTGCTACTACATGCTAGCA 4548
Db 585 GACAGACCTCCATCAAGAGAGCTACTGAAGCATCCAGTCTTTCTGCTACTACATGCTAGCA 644
QY 4549 ATTATGCAAGTCAACTACAGTAGTAAAGAGGATGCTCAACAGAGAAAAAACTTTGGG 4608
Db 645 ATTATGCAAGTCAACTACAGTAGTAAAGAGGATGCTCAACAGAG-CAAAACTTTTGTGGG 703
QY 4609 GAACACATTTGATTTCTACTGGCCATGATGCTGCAAGTATGCAAGGAGGAGGAGG 4668
Db 704 GAACACATTTGATTTCTACTGGCCATGATGCTGCAAGTATGCAAGGAGGAGGAGGAGG 763
QY 4669 GGGAAACCTTCACTAAGTATGTGATGCAAAATCATGATCTGTACTAAGCTCAGTAGTC 4728
Db 764 GGGAAACCTTCACTAAGTATGTGATGCAAAATCATGATCTGTACTAAGCTCAGTAGTC 823
QY 4729 AAAAGCCCA-ACCTAGTGCAGAACTGTAAACTGTGCTTCAAA 4772
Db 824 AAAAGTCCCAATTTGTGCAGAACTGTAAACTGTGCTTCAAA 868

RESULT 6
AL042445 653 bp mRNA linear EST 04-SEP-2003
LOCUS DKFp434D2221_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DEFINITION DKFp434D2221 5', mRNA sequence.
ACCESSION AL042445
VERSION AL042445.1 GI:5421814
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
AUTHORS This is the 5' sequence of the clone insert
TITLE Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
JOURNAL Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de;
COMMENT sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No 5' sequence available.
This clone (DKFp434D2221) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 868)

# REFERENCE AUTHORS TITLE JOURNAL COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth

Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11831 row: g column: 05

High quality sequence stop: 821.

Location/Qualifiers

## FEATURES

1..868

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="NMRI"

/db\_xref="taxon:10090"

/clone="IMAGE:5327644"

/tissue\_type="tumor, gross tissue"

/dev\_stage="5 months"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP Mam4"

/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Priscilla Furth,

NIH Reference for transgenic model: Li et al., Cell Growth

and Differentiation 7, 3-11 (1996)."

## ORIGIN

Query Match 11.1%; Score 583; DB 12; Length 868;

Best Local Similarity 85.0%; Pred. No. 3.6e-91;

Matches 664; Conservative 0; Mismatches 115; Indels 2; Gaps 1;

483 CGCGGTCGTGAGATGAGGATGAAGAACTCTCAAGGGTTGCACAAAGATGATGATCG 542

64 CGCGAATCGAGATGAGATGAAGAAACCTCAAGGACTGCACAGATGAGGATCG 123

543 TCCAGAGAACCAATGATCGAGGAGAACTGAAGCAACCTGTATGCCAGCTTGGAGCA 602

124 CCGGAGAGAGATGATCCGGGAGAGCTCAGGCGACCTGTATGCCGCTTGGAGCA 183

603 CGAATGTTGAAAGGAGAAATGCGAGGCGCTGTGTGTAACCAATCCAGTTAA 662

184 CGAGTGGTTGAGAGAGGAGAACAGAGAGGCCCTGTGGTGAAGCAATCCCTATTAA 243

663 AGGAGATGGATCTGAATGAATCACTTAGCAGCTGAGTCTCCAGGAGAGTCCAGGCAAG 722

244 AGGAGATGGATCTGAATGAATCACTTGGCAGCTGAGCCCCAGGAGAGGCGCCAGG 303

723 TCGGCTTCACAGCTTCCAAAGCGCGAGCGAGTCTTCTCTGCGAATCCCATCAGG 782

304 TTCGCTGCACAGCCCCCAAGGCGCGAGAGGCCATCTCTGCGAGCTCTCGTCAGG 363

783 TCGCACAGTGAATCAGAAATCTCCAGGAGTAGAAGAGAAAAGATTTCCCGAGTGCCTTT 842

364 GCGCTCGTGAAGCGGAATCCCGAGGAGTGAGACGGAACAGAGTCCCGGTGCCTTT 423

843 TCAGATGCGAGATCAACACCCCGAGAGCCCTTCACAGATGGCTTCTCACCATA 902

424 CCAGATGGCAGAAATCAACACCCCGAGAGCCCTTCACCGATGGCTTCTCCCGTA 483

903 TAGCCCTGAGGAAACAAACCCCGCTGTGTAAACAAGTGTATGCGGCCAGACTGTACT 962

484 CAGCCAGAGGAGAGCGAGCGCGCGGTGAACAAGTGTATGAGCCAGGCTGTACCTGCT 543

963 GCAGCAGATAGGCGCTAACTCTTCTGATTTGGAGAGAGAGCCAGCAATAAATACCG 1022

544 GCAGCAGATAGGAGCCCACTCTTCTGATTTGGAGAGAGAGTCCAGCAATAAATACCG 603

1023 GGTGTTTATTTGGGCGCTCAGAACTGCAGCTGTGCACGTGGAACATTTGTATTTCATCTGCT 1082

604 GGTGTTTATTTGGGCCACAGAACTGCAGCTGTGGCGTGGAGCATTTGTATTACCTCTT 663

1083 ATTGTGATCTCGGGTGTTCACATAGAACCTTCAGACCCCAATGTTATGGAGAAAAC 1142

664 GTTTGTATCTCGGGTGTTCAGCTTAGAAACCTTCAGCCCATGTTATGGAGAAAAC 723

1143 TTT--AAAGAATTTTTCAGGTTGAGAGTTTCTTCAGAAATATCACAGTAGGCGCTAGCTCA 1200

724 TTTTGAACATTTTCAGAGTTGAGAGTTTGTTCAGAAATATCACAGTAGGCGCTAGCTCG 783

1201 AGGATCAAGCTCCATCTCGTAACCATCCAGAGTTTGTTCAGCATGTCAATTTCT 1260

784 AGAATCAAGCTCCATCCCGGAACACCATCAGAAGTTGTCTCCGCGCTGGCAATGGT 843

1261 C 1261

844 C 844

RESULT 8

CA512935

LOCUS

DEFINITION

UI-R-FJ0-cqb-m-19-0-UI-r1 UI-R-FJ0 Rattus norvegicus cDNA clone

UI-R-FJ0-cqb-m-19-0-UI 5', mRNA sequence.

ACCESSION

CA512935

VERSION

CA512935.1 GI:25003889

KEYWORDS

EST.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 799)

Bonaldi,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)

Tissue Procurement: Dr. James Lin, University of Iowa

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics ([www.reagen.com](http://www.reagen.com)).

Seq primer: M13 REVERSE.

Location/Qualifiers

1..799

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-FJ0-cqb-m-19-0-UI"

/tissue\_type="embryo"

/dev\_stage="embryo"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-R-FJ0"

/note="Vector: pYX-Abs; Site 1: EcoR I; Site 2: Not I;

UI-R-FJ0 is a cDNA library containing the following

tissue(s): rat embryo. The library was constructed

## FEATURES source

according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTV73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (drl)18 tail. The sequence tag for this library is CATCTCTACT. This library was created for the University of Iowa Program for Rat Gene Discovery and Mapping (Val Sheffield, Bento Soares and Tom Casavant)"

ORIGIN

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Query Match      10.4%; Score 546.8; DB 14; Length 799;
Best Local Similarity 82.1%; Pred. No. 7.3e-85;
Matches 658; Conservative 0; Mismatches 125; Indels 18; Gaps 2;

QY 2729 TAGAGAAAACCTGGAAGAGGATTATGTCTACAAAATTGAGTGGCAGTTTCAGAGGACATTT 2788
DB      |||||
QY 2789 CTGAGAGACTGGCCAGCATTTTCAGTAGAGCTTCTAGTTCAACACACACACACACAA 2848
DB      |||||
QY 2799 CTGACAGACTGGCTGGGGTTTCTGTAGAGCTTCTAGTT-----CAGCAA 121
DB      |||||
QY 2849 CAACAGAGCAACCAAGCCATGTTTCAACAAAAGGCAGACCCACAGTCAGTGTGTA 2908
DB      |||||
QY 122 CAACAGACACCAAGCCACAGCTTCAACAAAAGGCAGACCCACAGTCAGTGTGTA 181
QY 2909 ACTCCTCTCCCTTATCATCATTCCTCCAAATTAATGTTTCCAGCTTGTCAACCCCTTCT 2968
DB      |||||
QY 182 ACTCCTCTCCCTTGTCTCTCTC-CTCAGTTAATGTTTCCAGCAATATCAGCCCCATGTT 238
QY 2969 CTTCTACCCCATCTGTACCACTGGCTGCACTGCAACAGATGCTCTTAAGCATAGACTTCAGG 3028
DB      |||||
QY 239 CATCTGCCCGCTGTCTGCCAGTGGCTCTGTAAACAGATGCTTCTAGCATAGACCTCGGG 298
QY 3029 GATTTCCTCTCGAGATACTCTTCTGCATCTCTCTCAAAACACAGCGCAAGTTTCTCTAC 3088
DB      |||||
QY 299 CGTTTGTCTCTGTAATAACCTCTCGCTCTCCCAACACAGCGCAAGTTTCTCCCTAC 358
QY 3089 AATTCCACAGAACTGTCTCTGAACCAAGACTCAGATAACTTCTCCAGTCTTTTACTC 3148
DB      |||||
QY 359 AGTTCCAGAGGACCTGTCTGTAGAACCGAGACTCAGAAAACCTCTCCCAAGTCTTTTACTC 418
QY 3149 AGTCAAGACCCCTTGCCCTTCCAGTAACATACACAGGCCCAAGCCATCTAGACCTACCCAG 3208
DB      |||||
QY 419 AGTCAGAGACCCCACTCCAGTAACATACACAGGCCCAAGCCATCTCCGACCCGTTCCGG 478
QY 3209 GTAATACAGTAACACAGGAGATCCCTCAAAAATAGCTGACACTTGTATGACAGTA 3268
DB      |||||
QY 479 GTAGACAAAGCAAACTAGGGGATGCCTCAAAAACAGCATGACACTCGACTGAACAGTG 538
QY 3269 GTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCAATAGTAGTAATGCTGTTATACCCA 3328
DB      |||||
QY 539 CTTCCAGTGTGATGACAGCTTTGGCAGTGGCAGCAACAGTGGCAGCGCGTCAATACCCA 598
QY 3329 GTGAGGAGACAGTGTTCACCCAGTAGAGGAGAAATGAGATTTAGTGTCAATACAGAGC 3388
DB      |||||
QY 599 GTGAGGAGACGCGCATTCACCCAGCAGAGGACAGTGCAGGTTAGTGTCAACCCCGAGC 658
QY 3389 TCAACTCCAGTATTGAGGACCTTCTTGAAGCATCTATGCGCTTCAAGTGTATCAACAGTAA 3448
DB      |||||
QY 659 TCACTCCAGTATCGAGACCTTCTTGAGGATCTATGCTTCAAGTGTACACACAGTCA 718
QY 3449 CTTTAAAGTGAAGTCTGTCTCTCTCTGAAAAGGCTGAAAATGATGATACCTTACA 3508
DB      |||||
QY 719 CTTTCAAGTGAAGTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 778
QY 3509 AAGATGATGTGAATCATATTC 3529
DB      |||||
QY 779 NAGATGAGCTCATCACATC 799
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RESULT 9
AJ450706
LOCUS      AJ450706 riken1 Gallus gallus cDNA clone 26c20r1, mRNA sequence.
DEFINITION      AJ450706 riken1 Gallus gallus cDNA clone 26c20r1, mRNA sequence.
ACCESSION      AJ450706
VERSION      AJ450706.1 GI:20217927
KEYWORDS      EST.
SOURCE      Gallus gallus (chicken)
ORGANISM      Gallus gallus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
REFERENCE      1 (bases 1 to 716)
AUTHORS      Buerstedde,J.M.
TITLE      Gallus gallus bursal lymphocyte EST
JOURNAL      Unpublished (2002)
COMMENT      Contact: Buerstedde JM
              Cellular Immunology
              Heinrich-Pette-Institute
              Martinistr. 52, 20251 Hamburg, Germany
              Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
              Location/Qualifiers
                1..716
                  /organism="Gallus gallus"
                  /mol_type="mRNA"
                  /db_xref="taxon:9031"
                  /clone="26c20r1"
                  /cell_type="bursal lymphocyte"
                  /dev_stage="2-3 weeks old"
                  /clone_lib="riken1"
                  /note="CB inbred strain"

FEATURES
            source
            1..716
              Query Match      10.4%; Score 544; DB 9; Length 716;
              Best Local Similarity 85.8%; Pred. No. 2.2e-84;
              Matches 615; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

QY 3546 GATGGAAGCTGAAGAAGAGAGCTTTAGCAATTCGCCATGGCAATGTGAGCGTCTCAGA 3605
DB      |||||
QY 3606 TGCCCTCCCCCTAGTTCCTCAGCTCGAGTGAATGAAATGGAAGATATCATCATTTTCA 3665
DB      |||||
QY 61 TGCCCTGCCAATAATTCGCCAACTACAGTGAATAATGTTGAGATATCATTAATTATCA 120
QY 3666 ACAGGATACACAGAGACTCTTACCAGGACATACCAAGCAAAACCAACCGTATAGAGAAGA 3725
DB      |||||
QY 121 GCAGGATACACAGAAACTCTGCTGGACATACCAAGCAAAAGCATATTACAGGGAAGA 180
QY 3726 CACTGATGCTGAAAGTCAACAGATAGGCTTGGAGCATTTCTCTTGTATCAGC 3785
DB      |||||
QY 181 TGCAAGATGGCTTAAAGGTCAGCAATTTGGTCTTGAGGCTTTCTCTCTGTTTCAAGC 240
QY 3786 TCAAGATGTGGAACTGGAACTTTAATGGCTGTTAAACAGGTGACTTATGTGAGAAACAC 3845
DB      |||||
QY 241 TCAAGATGTAGGAACAGGGACATTAATGGCTGTTAAACAGGTGACATATGTGAGGAACAC 3905
QY 3846 ATCTTCTGAGCAAGAAGTAGTAGAGCACTAAGAGAGAGATAGAGATAGATGAGCA 3965
DB      |||||
QY 301 ATCATCTGAGCAAGAAGAGGTAGTGGAGCACTAGAGGAGGAAATACCGATGATGATCA 360
QY 3906 TCTGAATCATCCAAACATCATTTAGATGTTGGAGCCACGCTGTGAGAGAGCAATTACAA 3965
DB      |||||
QY 361 TCTAAACCATCTAATATATTTCGCATGTTGGTGCTACATGTGAGAGAGCACTACAA 420
QY 3966 TCTTTTCATTAATGATGGCAGGGGATCGGTGGCTCATTTTGTGAGTAATATGAGC 4025
DB      |||||
QY 421 CCTCTTCATTAATGATGGCAGGGGATCAGTTCTCTCATTTTGTGAGTAATATGAGC 480
QY 4026 CTTCAAGAAATCAGTAGTTATTAACTACACTGAAAGTTACTCCGTCGGCTTTCTCTATCT 4085
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Db      481  CTTCAAGAAATCAGTTATTATTAACACAGAGCAACAGTTCAGTGGCCCTTTCTTACCT 540
Qy      4086  CCATGAAACCAATATTCACAGAGATGTCAAAAGGTGCCAATTTGCTAATTCAGACGAC 4145
Db      541  CCATGAGATCAGATAATTCATAGAGATGTCAAAAGGTGCCAATTTGCTAATTCAGACGAC 600
Qy      4146  TGGTCAGAGACTAGAATTCAGATTTTGGAGCTGCGAGCCAGGTGGCATCAAAAGGAAC 4205
Db      601  AGGTATAGATTAAGAATTCGTGATTTTGGAGCTGCGAGCCAGGTGGCATCAAAAGGAAC 660
Qy      4206  TGGTCAGAGAGATTTTCAAGGACAAATTAAGTGGGACAAATTTGCAATTTATGGCACTGA 4262
Db      661  TGGTCTGGGAGTTTCAAGGACAGTTT-GTGGGACTATTGCAATTTATGGCCCGGA 716

RESULT 10
AW499603
LOCUS
DEFINITION
  UI-HF-BPop-ain-b-12-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone
IMAGE:3072335 5', mRNA sequence.
ACCESSION
  AW499603
VERSION
  AW499603.1 GI:7111428
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 530)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgabs-r@mail.nih.gov
  Eco RI site shown at the beginning of the sequence.
  Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
  cDNA Library Preparation: M.B. Soares Lab
  cDNA Library Arrayed by: M.B. Soares Lab
  DNA Sequencing by: M.B. Soares Lab
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www.bio.llnl.gov/bbrp/image/image.html
  Seq primer: M3 Forward.

FEATURES
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    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:3072335"
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    /cell_type="germinal center B cells"
    /cell_line="MGC85"
    /lab_host="DH10B (LTI)"
    /clone_lib="NIH MGC 51"
    /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
    Constructed from size fractionated cytoplasmic mRNA
    (4.4-7.4kb). Directionally cloned. Cells provided by
    Louis M. Staudt, Ph.D. Library preparation by Maria de
    Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
  Query Match 9.9%; Score 519.8; DB 10; Length 530;
  Best Local Similarity 99.6%; Pred.No. 3.7e-80;
  Matches 521; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2268  TCTTGGCCGCTTGTCTTATAGATAGATGTTTGGGAATTCCTGCTGAATTTATCC 2327
Db      8      TCTTGGCCGCTTGTCTTATAGATAGATGTTTGGGAATTCCTGCTGAATTTATCC 67
Qy      2328  TCATATTGTCAGTACTGATGTTTCAAGCTGAGCTGTTGAAATCAGGTATAAGAGCT 2387
Db      68      TCATATTGTCAGTACTGATGTTTCAAGCTGAGCTGTTGAAATCAGGTATAAGAGCT 127
Qy      2388  GCTGTCCCTCTTAACCTTTCCTTGGAGTCCATTGATTAATCCCACTCAATGTTGGCAA 2447

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Db      128  GCTGTCCCTCTTAACCTTTCCTTGGAGTCCATTAAATTTCCACATCAATGGTTGGCAA 187
Qy      2448  ACTTTCCAGAGAGATCTACTTGGAGTCTTGOAAGATGGTTACTACAGTACCCCATGTGT 2507
Db      188  ACTTTCCAGAGAGATCTACTTGGAGTCTTGOAAGATGGTTACTACAGTACCCCATGTGT 247
Qy      2508  TTCAAAACCTGTTAGAAATGCTGAGTGTTCAGATTTCCACTCAGTTCACAGGATGCGTCG 2567
Db      248  TTCAAAACCTGTTAGAAATGCTGAGTGTTCAGATTTCCACTCAGTTCACAGGATGCGTCG 307
Qy      2568  CGGTTTGATGGCTATTCAGATGAGGTGAAATTCGCGAAGCCATCCAGTGGGCGTAGA 2627
Db      308  CGGTTTGATGGCTATTCAGATGAGGTGAAATTCGCGAAGCCATCCAGTGGGCGTAGA 367
Qy      2628  AGACACTTTGGATGCTCAACAGGACAGCTTCTTGAGGACATCTGTTCACCACTATCT 2687
Db      368  AGACACTTTGGATGCTCAACAGGACAGCTTCTTGAGGACATCTGTTCACCACTATCT 427
Qy      2688  GGAACCCACAGAGACAGTTCCTGAGTGACAGTCCATTTAGAGAAAACCTGGAAAAGG 2747
Db      428  GGAACCCACAGAGACAGTTCCTGAGTGACAGTCCATTTAGAGAAAACCTGGAAAAGG 487
Qy      2748  ATTATGCTGTACAAATTCAGTGCAGTTCAGGACATCTTCAGGACATTTCT 2790
Db      488  ATTATGCTGTACAAATTCAGTGCAGTTCAGGACATTTCT 530

RESULT 11
CF143161
LOCUS
DEFINITION
  UI-HF-BPop-ags-f-01-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
IMAGE:3101688 5', mRNA sequence.
ACCESSION
  CF143161
VERSION
  CF143161.1 GI:3258605
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 526)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  97044477
  8889548
  Contact: Soares, MB
  Coordinated Laboratory for Computational Genomics
  University of Iowa
  375 Newton Road, 4155 MEBRF, Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: bento-soares@uiowa.edu
  Tissue Procurement: Louis Staudt
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/humanfl.html
  Seq primer: PYX-5
  Location/Qualifiers
    1..526
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    /mol_type="mRNA"
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    /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;

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RESULT 13
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ACCESSION BI656574.1 GI:15570810
VERSION BI656574.1
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 719)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11835 Row: 0 Column: 06
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Library constructed by Life Technologies. Investigators
Providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
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## ORIGIN

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Query Match          9.6%; Score 504; DB 12; Length 719;
Best Local Similarity 85.5%; Pred. No. 2.1e-77;
Matches 561; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
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Db      244 AGAGATGGATCTTGAATGAATCACTTAGCAGCTGAGTCCAGCCCGAGGAGAGGCGCAGG 303
Qy      723 TCGGCTTCCAGAGCTCCAAAGGCGAGGCGAGCTCTCTCTGGCAACTCCGCCATCAGG 782
Db      304 TCCGCTGCGACCGAGCCCGGAGGCGAGCGAAGCCCATCTCTCTGGCAGCTCTCCGTCAGG 363
Qy      783 TCGCACAGTGAATTCAGAAATCTCCAGAGTAAAGAGAAAGAGTTTCCAGTGCCTTT 842
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Qy      1083 ATTGTGATGCTCGGGTGTTCACACTAGAACCTTCAGACCCATGTATTGGAGAA 1138
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AGENCOURT_15183146 NICHD_XGC_Emb4 Xenopus laevis cDNA clone
IMAGE:5514919 5', mRNA sequence.
CF287689
CF287689.1 GI:33647468
EST.
Xenopus laevis (African clawed frog)
Xenopus laevis
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 773)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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## RESULT 14

CF287689

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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High quality sequence stop: 715.

Location/Qualifiers

## FEATURES

source

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Technologies. Note: This is a Xenopus Gene Collection  
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## ORIGIN

Query Match 9.5%; Score 500.8; DB 14; Length 773;  
Best Local Similarity 78.7%; Pred. No. 7.5e-77;  
Matches 598; Conservative 0; Mismatches 162; Indels 0; Gaps 0;  
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QY 3869 TAGAAGCACTAAGAGAAGATAGAATGATGAGCCATCTGAATCATCCAAACATCATTA 3928  
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QY 3989 GGGATCGGTGGCTCATTTGCTGAGTAATATGAGGAGCTTCAAAGAATCAGTAGTTATTA 4048  
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## RESULT 15

EX485112

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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DKFP686N20245\_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

DKFP686N20245\_5', mRNA sequence.

EX485112 GI:31947543

EST.

Homo sapiens (human)

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 499)

Bloeker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,

Robo, G., Han, M., and Wiemann, S.

EST (Bloeker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., et al.)

Unpublished (2003)

Contact: MIPS

MIPS

Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;

sequenced by GBF (National Research Centre for Biotechnology Ltd.,

Braunschweig/Germany) within the cDNA sequencing consortium of the

German Genome Project.

No sl sequence available.

This clone (DKFP686N20245) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

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1. .499

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cDNA-collection"

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Db	481	CACAGAGACAGTTCCCT 499	

Search completed: May 14, 2004, 23:54:19  
Job time : 12084 secs







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D <sub>b</sub>	2041	CAGCTGTCCATATCAACAACACTGTGTGGAACTGTGCMAAGGCCAAAGGAGAGTGTCAGATT	2100
Q <sub>y</sub>	2164	GGCAGAGAAATACTAAAAGCTGGATCCATTTGGTGTATTTGGTGTGTGATTAATCTCTTAAT	2223
D <sub>b</sub>	2101	GGCAGAGAAATACTAAAAGCTGGATCCATTTGGTGTATTTGGTGTGTGATTAATCTCTTAAT	2160
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Q <sub>y</sub>	2524	ATGCTGAGTGTMTCCAG---TTCCACACTCATTCCACAGGATGGTGCOCGTTTGATGGCT	2580
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D <sub>b</sub>	3001	TCTCCTCAAAACACAGCGGCAAGTTTTTCTCTCAAAATTCACAGAAATCTGCTGAANAACAA	3060

QY	3118	GACTCAGATAAACTTTCCCGAGCTCTTTACTCAGTCAAGACCCCTTCCGCTCCAGTAACATA	3177
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QY	3178	CACAGGCCAAAGCCATCTAGACCTTACCCAGGTAAATACAAGTAAACAGGGAGATCCCTCA	3237
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DB	3181	AAAAATAGCATGACACTTGATCTGAAACAGTAGTTCCTCAATGTGATGACAGCTTTGGCTGT	3240
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DB	3961	TATGGAGCCTTCAAGAAATCTGATAGTTATTAACTACACTGAAACAGTTACTCCCGTGGCCTT	4020
QY	4078	TCGTATCTCCATGAAACCAAAATCATTCACAGAGATGTCAAAAGGTGCCAATTTGCTAATT	4137
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DB	4081	GACAGCACTGCTCAGAGACTTAAGAAATTTGCAGATTTTGGAGCTGCAGCCAGTTGGCATCA	4140

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DB 4141 AAAGAACTGGTCAGGAGAGTTTTCAGGGAACAATTACTGGGGAACAATTGCAATTTATGGCA 4200  
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DB 4201 CCTGAGTACTAAGAGGTCAACAGTATGGAAGAGCTGTGATGTATGGAGTGTGGCTGT 4260  
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DB 4261 GCTATTATAGAAATGGCTTGTGCAAAACCACTGGAATGCAAGAAACCACTCAATCAT 4320  
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DB 4321 CTTGCTTTGATTTAAGATGCTAGTGAACACTACTGCTCCATCGATCCCTTCACATTGG 4380  
QY 4438 TCTCCTGGTTTACAGATGCTGCTTCTGTTGTTTGAAGACTTCAACCTCAGGACAGACCT 4497  
DB 4381 TCTCCTGGTTTACAGATGCTGCTTCTGTTGTTTGAAGACTTCAACCTCAGGACAGACCT 4440  
QY 4498 CCATCAAGAGAGTACTGAAGCATCCAGTCTTTCGTACTACATGCTGATGCAATTTATGCG 4557  
DB 4441 CCATCAAGAGAGTACTGAAGCATCCAGTCTTTCGTACTACATGCTGATGCAATTTATGCG 4500  
QY 4558 ATCAACTACAGTACAGAAACAGATGCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAG 4617  
DB 4501 ATCAACTACAGTACAGAAACAGATGCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAG 4560  
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DB 4561 TGATATTTCTACTGGCATGATGCACTGAACAGATGTAAGAGAGAGAGAGAGAGAGAGAG 4620  
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DB 4801 TCAGCAATATTAGCGGCTGAGGGGCTCAGGATCTATTTTAAATTTATTTTCTTTCCCA 4860  
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DB 4861 TTTTATATAGTATCACAAGAGAGGGGTTCTGCAATTCGTTTCAATTTTGTCTACTGG 4920  
QY 4978 CTATAAATCAGTATCTGCTCTTTTAGGTCAAGATGCTATGATGATGATGATGATGATG 5037  
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DB 5041 CCAGGAGAGTGTGGCTCAATTTGCAATTTTACTGTTGGCCCAATTCATTTGCTTTTGA 5100  
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QY 5218 ATCTTTTTTTTCAAAACCAAAAAA 5245  
DB 5161 ATCTTTTTTTTCAAAACCAAAAAA 5188

RESULT 2  
US-10-433-794-26  
; Sequence 26, Application US/10433794  
; Publication No. US20040077044A1  
; GENERAL INFORMATION:  
; APPLICANT: YUE, Henry; DING, Li;  
; APPLICANT: LAL, Preeti G.; GRIFFIN, Jennifer A.;  
; APPLICANT: GURURAJAN Rajagopal; BAUGHN, Mariah R.;  
; APPLICANT: ISON, Craig H.; RAMKUMAR, Javalaxmi;  
; APPLICANT: TRIBOULEY, Catherine M.; SWARNAKAR, Anita;  
; APPLICANT: BURFORD, Neil; BANDMAN, Olga;  
; APPLICANT: THORNTON, Michael; KHAN, Farrah A.;  
; APPLICANT: WALIA, Narinder K.; NGUYEN, Damiel B.;  
; APPLICANT: ELLIOTT, Vicki S.; XU, Yuming;  
; APPLICANT: LU, Yan; HAPALIA, April J.A.;  
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;  
; APPLICANT: ARVIZU, Chandra S.; FORSYTHE, Ian J.  
; TITLE OF INVENTION: KINASES AND PHOSPHATASES  
; FILE REFERENCE: PI-0311 USN  
; CURRENT APPLICATION NUMBER: US/10/433.794  
; CURRENT FILING DATE: 2003-06-04  
; PRIOR APPLICATION NUMBER: PCT/US01/47431  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: US 60/254,034  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,814  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/255,756  
; PRIOR FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: US 60/256,172  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: US 60/257,416  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 60/260,912  
; PRIOR FILING DATE: 2001-01-10  
; PRIOR APPLICATION NUMBER: US 60/264,644  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: US 60/266,017  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PERL Program  
; SEQ ID NO 26  
; LENGTH: 4858  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 7198931CBI  
US-10-433-794-26  
Query Match 90.5%; Score 4744.8; DB 17; Length 4858;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 4793; Conservative 0; Mismatches 22; Indels 5; Gaps 3;  
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DB 1 ATGCGCGCGCGCGCGGGAATCGCGCTCTGCTGGGATTCGCGGCCCGCGGCTAG 60  
QY 67 AGCCCTGAGGAGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126  
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QY 127 GCAGGAGTCTGCGGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 186  
DB 121 GCAGGAGTCTGCGGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
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DB 181 CAGTGGCAAGTGGGAGTGGAGCTGGAGCTGGACCTGCTGAGCAGAGAGAGAGAG 240  
QY 247 GCGGCTTACCGCGGCTCTCTCGACTTCCCTCCGAGAGAGAGAGAGAGAGAGAGAG 306  
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QY 307 AGTGGGACCGGCTTCCAGCCTGTGGCGGTGCGCGCGCGCCGCCACCGAGCGCGGCGCGC 366  
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Db 421 GCCGAGCCCGGGGAGAGCGCGCGCGCGCGCGCGCGCGCTCTCGAGCGCGCGCGCGC 480  
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Db 541 GAGGAAAGATGATCAGGGGAGAACTGAGAGCAACCTGTATGCGAGCGCTGGAAGCAGGAA 600  
QY 607 TGGTTGAAAGGAGAAATAGCGAGGCGCTGTGTGTGTAAACCAATCCCAAGTTAAAGGA 666  
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QY 667 GATCGATCTGAAATGAATCACTTAGAGCTGAGTCTCCAGAGAGGTCCAGGCAAGTGGC 726  
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Db 1141 AAGAAATTTGAGTTGAGAGTTTGTTCAGAAATATCACAGTAGCGGTAGCTCAAGGATC 1200  
QY 1207 AAGCTCCATCTCGTAAACCATCCAGAAAGTTGTTTCAAGCATGTCAAAATCTCATACA 1266  
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Db 1441 AGAAATAGAGAAACCTTTAATATGTCCCTTTGTAGATCTAAGTGGAGATCTCATGATTTTC 1500  
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QY 1567 CAAACCGTACAGCAGCAGCCTTTGGCTGGATCAAGAGAAATCAAGAGCAATTTTAAAC 1626  
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QY 1927 ATGGCTGTGCTGACCTGTCTACAAAGTGTACGTGTCTTTTAAAAACATTTGAGAGCC 1986  
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QY 2467 TTGAGTTCTGCAAGAATGGTTACTACAGTACCCTATGTGTGTTCATAAACTGTTAGAAATG 2526

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2527	CTGAGTGTTCAGAGTTCACCTCACTTCCACAGGATGGTCGGTGTGATGGCTATTGCA	2586	3607	GCCTCCCATATAGTTCTCCTCAGCTGCAGGTTGAAAATGGAGAAGATATCATCATTTATTCAA	3666
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2587	GATGAGTGGAAATTCGCAAGCCATCAGTTGGCGTGAAGACACTTTGAGTGTCAA	2646	3667	CAGGATACACAGAGACTCTACCGAGCATACCAAGCAAAACCAACCTATAGAGAAGAC	3726
2581	GATGAGTGGAAATTCGCAAGCCATCAGTTGGCGTGAAGACACTTTGAGTGTCAA	2640	3658	CAGGATACACAGAGACTCTACCGAGCATACCAAGCAAAACCAACCTATAGAGAAGAC	3717
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2641	CAGGACAGCTTCTGACGGCATCTGTTCCCAACCACTATCTGGAACCCACAGAGACAT	2700	3718	ACTGAATGGCTGAAGGTCACACAGATAGGCTTTGGAGCATTTTCTTCTTGTATCAGGCT	3777
2707	TCCCTGAGTGCAAGTCCATTTAGAGAAACTCGAAAAGATATGTGCTACAAAATTG	2766	3787	CAAGATGTGGAACTCGAACTTTAATGGCTGTAAACAGGTGACTTATGTTCAGAAAACACA	3846
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2767	AGTGCCAGTTTCAGAGCAATTTCTGAGAGACTGGCCAGCATTTTCAGTAGGACCTTCATG	2826	3847	TCCTCTGAGCAAGAGAGTAGTAGAGCACTTAGAGAGAGAGATAGAAATGATGAGCCAT	3906
2761	AGTGCCAGTTTCAGAGCAATTTCTGAGAGACTGGCCAGCATTTTCAGTAGGACCTTCATG	2820	3838	TCCTCTGAGCAAGAGAGTAGTAGAGCACTTAGAGAGAGAGATAGAAATGATGAGCCAT	3897
2827	TCAC	2886	3907	CTGAATCATCCAAACATCATTTAGGATTTGGGAGCCAGCTGTGAGAGAGAGCAATTTACAAT	3966
2821	T---CAAC	2877	3898	CTGATCATCCAAACATCATTTAGGATTTGGGAGCCAGCTGTGAGAGAGAGCAATTTACAAT	3957
2887	AGACCCCAAGTCAGTGTGTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2946	3967	CTCTTCATTAATGAGTAGGAGGAGGATCGTGGCTCATTTTCTCTCAGTAATATGAGGCC	4026
2878	AGACCCCAAGTCAGTGTGTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2937	3958	CTCTTCATTAATGAGTAGGAGGAGGATCGTGGCTCATTTTCTCTCAGTAATATGAGGCC	4017
2947	CGAGCCTGTCAACCGCTTCTCTCTACCCCATCTGTACAGCTGCACATGCAACAGAT	3006	4027	TTCAAGAAATCAGTAGTATTAACTACACTGAACAGTTTACTCCGTGGCTTTCTGTATCTC	4086
2938	CGAGCCTGTCAACCGCTTCTCTCTACCCCATCTGTACAGCTGCACATGCAACAGAT	2997	4018	TTCAAGAAATCAGTAGTATTAACTACACTGAACAGTTTACTCCGTGGCTTTCTGTATCTC	4077
3007	GTCTTAAGCATAGACTTCAGGGAATTCATTCCTGAGCAATACCTTCTGATCTCTCTCAA	3066	4087	CATGAAAACCAATCATTCACAGAGATGTCAAGGTGCCAATTTCTCTATTCACAGACACT	4146
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3178	AAGCCATCTAGACCTACCCAGTAAATCAAGTAAACAGGAGATCCCTCAAAAATAGC	3237	4258	CTAAGAGCTCAACAGTATGGAAGAGCTGTGATGTATGGAGTGTGGCTGTGCTATTATA	4317
3247	ATGACACTTGATCTGAACAGTATGTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCAAT	3306	4327	GAATGCTGTGTGCAAAACCAACCACTGGAATGCAAGAAAACACTCCCAATCATCTTGCTTTG	4386
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3367	AGATTAGATGCAATACAGAGCTCAACTCCAGTATGAGGACCTTCTTGAAGCATCTATG	3426	4447	TTACGAGATGGGCTCTTCTGTTGTTAGAACTTCAACCTCAGGACAGAGCCTCCATCAAGA	4506
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3487	GCTGAAATGATGATACCTCAAAAGATGATGTAATCATATCATCAAAAGTGCAGAGAGAG	3546	4567	AGTAGAAAACAGATGCTCAACAGAGAAAAAAACTTGTGGGAAACCAATTGATATTTCT	4626
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3547	ATGGAAGCTGAAGAGAGAGCTTTTAGCAATTTGCCATGGCAATGTGCAGCGTCTCAGGAT	3606	4627	ACTGGCCATGATGCACTGAACAGACTATGAACAGGCGCATGTGGGAAACCTTACCTTAAGT	4686
			4618	ACTGGCCATGATGCACTGAACAGACTATGAACAGGCGCATGTGGGAAACCTTACCTTAAGT	4677











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APPLICANT: Wang, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No US20040404824A1el Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIORITY APPLICATION NUMBER: US 09/488,725
PRIORITY FILING DATE: 2000-01-21
PRIORITY APPLICATION NUMBER: US 09/491,404
PRIORITY FILING DATE: 2000-01-25
PRIORITY APPLICATION NUMBER: US 09/496,914
PRIORITY FILING DATE: 2000-02-03
PRIORITY APPLICATION NUMBER: US 09/515,126
PRIORITY FILING DATE: 2000-02-28
PRIORITY APPLICATION NUMBER: US 09/519,705
PRIORITY FILING DATE: 2000-03-07
PRIORITY APPLICATION NUMBER: US 09/540,217
PRIORITY FILING DATE: 2000-03-31
PRIORITY APPLICATION NUMBER: US 09/552,929
PRIORITY FILING DATE: 2000-04-18
PRIORITY APPLICATION NUMBER: US 09/577,408
PRIORITY FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: dt_FL_genes Version 5.0
SEQ ID NO 512
LENGTH: 4696
TYPE: DNA
ORGANISM: Homo sapiens
US-10-112-944-512

Query Match 87.1%; Score 4569; DB 13; Length 4696;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 4657; Conservative 0; Mismatches 30; Indels 10; Gaps 6;

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DB 62 CCGGGGAGCTGCTCGGGAGGCGGCGGAGCGGGGGCGCGAGCGGGCGGAGCTGGCGGCGG 121
QY 185 GGCAGCTGCGCAAGTGCAGGTGTGAGCTGAGCTGAGCAGAGTGCCTGAGCAGCGCTTTC 244
DB 122 GGCAGCTGCGCAAGTGCAGGTGTGAGCTGAGCTGAGCAGCGCTTTC 181
QY 245 TTGCGGCTCACCGCGGCTCTCTCGACTTCCCGTCCCGGAGCGCGGAGCGCGAGCGG 304
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QY 305 GGAGTGGACCGGCTTCCAGCCTGTGCGGTGCGCGGCCCGCCACGAGCGCGAGCGCGG 364
DB 242 GGAGTGGACCGGCTTCCAGCCTGTGCGGTGCGCGGCCCGCCACGAGCGCGAGCGCGG 301
QY 365 GCGGCGGCGGCTTACCGAGTTCGGTGGCGGCGGAGCGGCGGCTCGAGTCCCGCGAG 424
DB 302 GCGGCGGCGGCTTACCGAGTTCGGTGGCGGCGGAGCGGCGGCTCGAGTCCCGCGAG 361
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DB 362 CCGGCGGAGCGCGGAGAGCGGCGGCGGCGGCGGCGGCTCTCTGAGCGGCGGCGG 421
QY 485 CCGGTGCTGAGATGGAGATTAAGAACTCTCAAGAGGTTGCAAGATGATGATGCTC 544
DB 422 CCGGTGCTGAGATGGAGATTAAGAACTCTCAAGAGGTTGCAAGATGATGATGCTC 481
QY 545 CAGAGGAACGAATGATCAGGAGAGAACTGAAGGCAACTCTGATGCCAGCGCTGGAAGCAG 604
DB 482 CAGAGGAACGAATGATCAGGAGAGAACTGAAGGCAACTCTGATGCCAGCGCTGGAAGCAG 541
QY 605 AATGTTGGAAAGGAGAAATAGGCGAGGGCGCTGTGGTGTGTTAAACCAATCCAGTTAAG 664
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Db 1682 GAGAGATGGCCCTCAGCGCTCTTCCCATGATGTCAGTGGGCGCCCTGCTGTTGCAAAATG 1741  
Qy 1805 GGGAGAGCACTGGAAATTTCTGGGCGCAGCAGTGGAAAGCAGCCCGAGTGGGGAGGCCACCA 1864  
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Qy 1865 GTGGGTCTCCAGACCACTATCTCAGAGATGTGGTGGAGGATGCTGTCAGCGTCTGT 1924  
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Qy 1925 CAATGCTGTGCTGACCCCTGTCTACAAAGTGTACGTGTGCTTTTAAACCACTTGGAG 1984  
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Qy 1985 CCATGCTGGTATATCTCTCTGACAGTGTAGGCGGAAGAACTCAAACTTCAGAGACTTC 2044  
Db 1922 CCATGCTGGTATATCTCTCTGACAGTGTAGGCGGAAGAACTCAAACTTCAGAGACTTC 1981  
Qy 2045 TCCAGCCAGTGTAGACCACTCTAGTCAAAATGTGAGATGGCAATAGCGCGCACCAAGTC 2104  
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Qy 2759 CAAAATTGATGCCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGCAATTTCACTAGGAC 2818  
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Qy 3719 GAGAGACACTGAATGGCTGAAAGGTCAACAGATAGGCTTCGAGCATTTCTTCTTGT 3778  
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Qy 3839 GAAACACTCTCTGAGCAGAGAGAGTAGTAGACACTTAAGAGAGAGAGATGAATGA 3898  
Db 3782 GAAACACTCTCTGAGCAGAGAGAGAGTAGTAGACACTTAAGAGAGAGAGATGAATGA 3841



QY 845 AGAGTGGCAGAAATCACACCACCCGGAAGAGCCCTTCCACAGATGGCTTCTCACCATATA 904  
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QY 1025 TGTATTATGGCCCTCAGAACTGACGTGTGACCTGGGACATCTCTGATTATCACTCTGTAT 1084  
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Db 1802 GTGGGTCTCCAGACAGTATCTCAGGAGATGTGTTGGAGGATGTGTCGACCGTCTGT 1861

QY 1925 CAATGGTCTGCTGACCCCTGTCTACAAGTGTAGTTGCTGTCTTAAAAACATTGAGAG 1984  
Db 1862 CAATGGTCTGCTGACCCCTGTCTACAAGTGTAGTTGCTGTCTTAAAAACATTGAGAG 1921  
QY 1985 CCATGCTGGTATATCTCTCTGCGCAACAGTTTAGCGGAAAGAAATCAAACTTCAGAGACTTC 2044  
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QY 2045 TCAGCCAGTTGTAGACACCATCTCTAGTCAATGTGCAGATGCCAATAGCCGCAAGTC 2104  
Db 1982 TCAGCCAGTTGTAGACACCATCTCTAGTCAATGTGCAGATGCCAATAGCCGCAAGTC 2041  
QY 2105 AGCTGTCCATATCAACACACTGTTGGAACTGTGCAAAAGGCCAAGCAGAGTTGGCAGTTG 2164  
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QY 2405 TTGCTTTGAGTCCATGTGATAATTCCTCAATGGTGGCAAACTTCCAGAGAGATCT 2464  
Db 2342 TTGCTTTGAGTCCATGTGATAATTCCTCAATGGTGGCAAACTTCCAGAGAGATCT 2401  
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QY 2582 TTGAGATGAGTGGAAATGGCGAGCCATCCAGTTGGCGGTAGAGACACTTTTGGATG 2641  
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QY 2642 GTCAACAGGACAGC ---TTCTTTCAGGCACTCTGTTCCCAACAACTATCTGGAACCAAG 2699  
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QY 2700 GAACAGTTCCCT ---TGAGTGACAGTCCATTTAGAGAAACTGGAAAGGATTTATGCTA 2758  
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QY 2879 CAAAAGCAGACCCCAAGTTCAGTGTGAACTCTCTCTCTCTTATCTCATCATTCCTCAAT 2938  
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; DATABASE ENTRY DATE: 2001-06-18  
US-10-172-118-111

Query Match 87.0%; Score 4564.6; DB 13; Length 4693;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 4647; Conservative 0; Mismatches 39; Indels 9; Gaps 5;

QY	65	CGAGCCCTGAGGCGGCGGCGGAGGAGCCCTCAAGGCGAGCAGCGGCGGCGGCTG	124
DB	2	CGAGCCCTGAGGCGGCGGCGGAGGAGCCCTCAAGGCGAGCAGCGGCGGCGGCTG	61
QY	125	CCGCGGACCTGCTGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGAGCTGCGGCGG	184
DB	62	CCGCGGACCTGCTGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGAGCTGCGGCGG	121
QY	185	GGAGCTGCGGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGG	244
DB	122	GGAGCTGCGGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGG	181
QY	245	TTGCGGCTCACCAGCGGCGGCTCTCGACTTCCCGTCCCGGAGCGGCGGCGGAG	304
DB	182	TTGCGGCTCACCAGCGGCGGCTCTCGACTTCCCGTCCCGGAGCGGCGGCGGAG	241
QY	305	GGAGTGGAGCGGCTTCCAGCGCTGCGGCTGCGGCGGCGGCGGCGGCGGAGCGG	364
DB	242	GGAGTGGAGCGGCTTCCAGCGCTGCGGCTGCGGCGGCGGCGGCGGCGGAGCGG	301
QY	365	CGCGCGCCACCTTACCGAGTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGAG	424
DB	302	CGCGCGCCACCTTACCGAGTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGAG	361
QY	425	CGCGCGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	484
DB	362	CGCGCGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	421
QY	485	CGGTCGTGAGATGAGAAATAAAGAACTCTCAAGGAGGTTGCACAAGATGATGTC	544
DB	422	CGGTCGTGAGATGAGAAATAAAGAACTCTCAAGGAGGTTGCACAAGATGATGTC	481
QY	545	CAGAGAAACGAATGATAGGAGAACTGAAGGAACTGATGATGATGATGATGATG	604
DB	482	CAGAGAAACGAATGATAGGAGAACTGAAGGAACTGATGATGATGATGATGATG	541
QY	605	AATGTTGGAAGGAGAAATAGGCGGCGCTGTGTTGTTGTTGTTGTTGTTGTTG	664
DB	542	AATGTTGGAAGGAGAAATAGGCGGCGCTGTGTTGTTGTTGTTGTTGTTGTTG	601
QY	665	GAGATGGAATCTGAATGAATCACTTAGCAGTGTGATGATGATGATGATGATG	724
DB	602	GAGATGGAATCTGAATGAATCACTTAGCAGTGTGATGATGATGATGATGATG	661
QY	725	CGGCTTCCAGCTTCCAAAGCGGAGCGGCTTCTCTCTCTCTCTCTCTCTCTCT	784
DB	662	CGGCTTCCAGCTTCCAAAGCGGAGCGGCTTCTCTCTCTCTCTCTCTCTCTCT	721
QY	785	GCACAGTGAATCAGAACTCTCAGGAGTAAGGAGAAAGAGTTTCCCGAGTCTTTC	844
DB	722	GCACAGTGAATCAGAACTCTCAGGAGTAAGGAGAAAGAGTTTCCCGAGTCTTTC	781
QY	845	AGAGTGGAGATCACCACCGGAGGCGGCTTCCAGAGTGGCTTCTCACCATA	904
DB	782	AGAGTGGAGATCACCACCGGAGGCGGCTTCCAGAGTGGCTTCTCACCATA	841
QY	905	GGCCTGAGGAAACAAACCGCGCTGTAAACAAAGTATGCGGCGGAGCTTACTTC	964
DB	842	GGCCTGAGGAAACAAACCGCGCTGTAAACAAAGTATGCGGCGGAGCTTACTTC	901
QY	965	AGCAGTAGGCGCTAATCTTCTGATGAGGAGGAGCGGCGGAGCAATAATACCGG	1024
DB	902	AGCAGTAGGCGCTAATCTTCTGATGAGGAGGAGCGGCGGAGCAATAATACCGG	961
QY	1025	TGTTTATGGGCTCAGAACTGCGAGCTGCGAGCTGCGAGCACTCTGTATTCATCT	1084

DB	962	TGTTTATGGGCTCAGAACTGCGAGCTGTCAGATGTCAGATGTCAGATGTCAGAT	1021
QY	1085	TTGTGATGCTCCGGGTGTTTCACTAGAACCTTCAGACCCCAATGTTATGGAGAAA	1144
DB	1022	TTGTGATGCTCCGGGTGTTTCACTAGAACCTTCAGACCCCAATGTTATGGAGAAA	1081
QY	1145	TAAAGAAATTTGAGGTTGAGAGTTTGTTCAGAAATATCACAGTAGGCTAGCTCA	1204
DB	1082	TAAAGAAATTTGAGGTTGAGAGTTTGTTCAGAAATATCACAGTAGGCTAGCTCA	1141
QY	1205	TCAAGCTCCATCTCGTAACACCACTCAGAAAGTTTGTTCACGCAATGTCATA	1264
DB	1142	TCAAGCTCCATCTCGTAACACCACTCAGAAAGTTTGTTCACGCAATGTCATA	1201
QY	1265	CATTGTCATCATCTAGTACTTCTAGTCTAGTTCAGAAAACAGCAATAAAGATGA	1324
DB	1202	CATTGTCATCATCTAGTACTTCTAGTCTAGTTCAGAAAACAGCAATAAAGATGA	1261
QY	1325	TAACAGATGTCCTATTTGTTTGGGCACTGCTTGTATGAAGAAAGTCTTACAGT	1384
DB	1262	TAACAGATGTCCTATTTGTTTGGGCACTGCTTGTATGAAGAAAGTCTTACAGT	1321
QY	1385	AAGACGGCTGCGAGAAACAAAGCTGCAACCACTGATGTCATCAATTTGGGCA	1444
DB	1322	AAGACGGCTGCGAGAAACAAAGCTGCAACCACTGATGTCATCAATTTGGGCA	1381
QY	1445	GAAGAAATAGAGAACTTTTATGTCCTTGTAGATCTAAGTGGAGATCTCATGAT	1504
DB	1382	GAAGAAATAGAGAACTTTTATGTCCTTGTAGATCTAAGTGGAGATCTCATGAT	1441
QY	1505	TCTACAGCCACAGTGTCAAGTCTGTCCTTCCCTTCTTCCCTCAGAGTGCACAG	1564
DB	1442	TCTACAGCCACAGTGTCAAGTCTGTCCTTCCCTTCTTCCCTCAGAGTGCACAG	1501
QY	1565	AGCAACCGTACAGCAGCAGCTTTGGTGGATCAGAGGAATCAAGAGACCAATTTA	1624
DB	1502	AGCAACCGTACAGCAGCAGCTTTGGTGGATCAGAGGAATCAAGAGACCAATTTA	1561
QY	1625	ACCTTACTCATATGGAATCTCAGCAAACTCCCTCTCTCTTACAAAGATTTAGT	1684
DB	1562	ACCTTACTCATATGGAATCTCAGCAAACTCCCTCTCTTACAAAGATTTAGT	1621
QY	1685	GAATTCAGTGTGGAATGGAATCTGTCCTGCTTATTTCTAGAACTGGAATGTA	1744
DB	1622	GAATTCAGTGTGGAATGGAATCTGTCCTGCTTATTTCTAGAACTGGAATGTA	1681
QY	1745	GAGAGATGCGCTCAGGCGCTTTCCATGATGTCAGTGGGCGCTCTGTTGGCAATG	1804
DB	1682	GAGAGATGCGCTCAGGCGCTTTCCATGATGTCAGTGGGCGCTCTGTTGGCAATG	1741
QY	1805	GGAGAGCACTGGAATTTCTGGGCGCAGCAGTGAAGCAGCCGAGTGGGAGCCACCA	1864
DB	1742	GGAGAGCACTGGAATTTCTGGGCGCAGCAGTGAAGCAGCCGAGTGGGAGCCACCA	1801
QY	1865	GTGGGTCTTCCAGACCACTGATCTCAGGAGATGTTGTTGAGGATGCTGCGGTTCTGT	1924
DB	1802	GTGGGTCTTCCAGACCACTGATCTCAGGAGATGTTGTTGAGGATGCTGCGGTTCTGT	1861
QY	1925	CAATGTCTGTGTCACCTCTCTCAAAAGTGTACCTGCTTTTAAAAACATTGAGAG	1984
DB	1862	CAATGTCTGTGTCACCTCTCTCAAAAGTGTACCTGCTTTTAAAAACATTGAGAG	1921
QY	1985	CCATGTGTTATATATCTCTTCCACAGTTTACGCGAAAGAAATCAAACTTCAGAG	2044
DB	1922	CCATGTGTTATATATCTCTTCCACAGTTTACGCGAAAGAAATCAAACTTCAGAG	1981
QY	2045	TCCAGCCAGTTGTAGACCACTCTAGTCAATGTCAGATGTCATAGCGGCACAGTC	2104
DB	1982	TCCAGCCAGTTGTAGACCACTCTAGTCAATGTCAGATGTCATAGCGGCACAGTC	2041
QY	2105	AGCTGTCCATATCAACACTGTTGGAAGTGTGCAAGCGCAAGCAGGAGCTTGCAG	2164
DB	2042	AGCTGTCCATATCAACACTGTTGGAAGTGTGCAAGCGCAAGCAGGAGCTTGCAG	2101

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DB 2102 GCAGAGAAATCTAAAGCTGGATCCATTTGGTATTTGGTGTGTGATTAATGCTTAAAT 2161  
QY 2225 GTATTTCTGGAAACCAAACTGAATCAAACTTGGCAAGAACTTTCTGGCCGCTTTGTC 2284  
DB 2162 GTATTTCTGGAAACCAAACTGAATCAAACTTGGCAAGAACTTTCTGGCCGCTTTGTC 2221  
QY 2285 TTATAGATAGACTGTTGTTGGAATTTCTGCTGTAATTTATCTCATATTTGTCAGTACTG 2344  
DB 2222 TTATAGATAGACTGTTGTTGGAATTTCTGCTGTAATTTATCTCATATTTGTCAGTACTG 2281  
QY 2345 ATGTTTCAAGCTGAGCTGTTGAAATCAGGTATAGAGCTGCTGCTCCCTTTAACT 2404  
DB 2282 ATGTTTCAAGCTGAGCTGTTGAAATCAGGTATAGAGCTGCTGCTCCCTTTAACT 2341  
QY 2405 TTGCTTTGAGTCCATTTGATTAATTTCCCACTCAATGTTGCAAACTTTCCAGAGATCT 2464  
DB 2342 TTGCTTTGAGTCCATTTGATTAATTTCCCACTCAATGTTGCAAACTTTCCAGAGATCT 2401  
QY 2465 ACTTGAGTTCTGCAAGATGTTTACTACAGTACCCCATGTTTTCAAAACCTGTTAGAAA 2524  
DB 2402 ACTTGAGTTCTGCAAGATGTTTACTACAGTACCCCATGTTTTCAAAACCTGTTAGAAA 2461  
QY 2525 TGCTGAGTGTTCAG--TTCCACTCACTTCCAGGATGCGTCCGCTTTGATGGCTA 2581  
DB 2462 TGCTGAGTGTTCAGTGTTCCTCACTTCCAGGATGCGTCCGCTTTGATGGCTT 2521  
QY 2582 TTGAGATGAGTGGAAATTCGCAAGCCATCCAGTTTGGCGTAGAAGACACTTTGATG 2641  
DB 2522 ATGAGATGAGTGGAAATTCGCAAGCCATCCAGTTTGGCGTAGAAGACACTTTACAAC 2581  
QY 2642 GTCAACAGGACAGC--TTCTTGTGAGGATCTGTTCCCAACAATCTCTGGAACCAACA 2699  
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QY 2700 GAACAGTTTCCC--TGAGTGCACTGTCATTTAGAGAAATTCGAAAGGATTTGCTA 2758  
DB 2642 GAACAGTTTCCCCTTGAGTGCACTGTCATTTAGAGAAATTCGAAAGGATTTGCTA 2701  
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DB 2702 CAATAATGAGTGCAGTTTCAGAGACATTTCTGAGACTGGCAGCATTTCACTAGTAGGAC 2761  
QY 2819 CTTCTAGTTCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 2878  
DB 2762 CTTCTAGTTCAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 2821  
QY 2879 CAATAAGGACAGCCCAAGTGTGTTGAACTCTCTCTCTTATCTCATCTTCCCAAT 2938  
DB 2822 CAATAAGGACAGCCCAAGTGTGTTGAACTCTCTCTCTTATCTCATCTTCCCAAT 2881  
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DB 2942 CAACAGATGTTCTTAAGCATAGACTTCCAGGATTCATTTCCCTGAGAAATACCTTCTGCAT 3001  
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DB 3002 CTCCTCAACAACAGCGGAAGTTTCTCTAATAATTCACAGAACTGTCCTGAAACAAG 3061  
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DB 3062 ACTCAGATAAACTTTTCCCGAGTCTTTACTCAGTCAAGACCCCTTCCCTCCAGTAAACATAC 3121  
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DB 3842 TGAGCCATCTGAATCATCCAAACATCATTAGAGATTTGGAGCCACCTGTGAGAGAGCA 3901  
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DB 3902 ATTACATCTCTTCAATGATGCGCAGGGGATCGGTGGCTCATTTTGTGAGTAAAT 3961  
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DB 3962 ATGAGGCTTCAAGAGATCAGTAGTTTAACTACTGAGAGAGTACTCCGTTGGACTTT 4021  
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DB 4202 CTGAGGTACTAAGAGGTCAACAGTATGAGAGAGCTGTGATGTATGAGTGTGGCTGTG 4261  
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Qy 4739 ACTAGTGCAGAACT 4753  
Db 4679 ACTAGTGCAGAACT 4693

## RESULT 7

US-10-152-319A-2042  
; Sequence 2042, Application US/10152319A  
; Publication No. US20040072160A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Higgs, Brandon  
; APPLICANT: Castile, Arthur  
; APPLICANT: Elashoff, Michael  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5089-US  
; CURRENT APPLICATION NUMBER: US/10/152,319A  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 60/292,335  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/297,523  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,810  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,807  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,808  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/315,047  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: US 60/324,928  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/330,867  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/330,462  
; PRIOR FILING DATE: 2001-10-22  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2221  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2042  
; LENGTH: 5180  
; TYPE: DNA

; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. NM\_053887  
US-10-152-319A-2042

Query Match 65.2%; Score 3420.8; DB 12; Length 5180;  
Best Local Similarity 84.5%; Pred. No. 0;  
Matches 4020; Conservative 0; Mismatches 647; Indels 91; Gaps 12;

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Db 570 GCGCGAGCCCCGAGCGCGCGCGCGCGGAGCTCTCCAGGAGAGCGCGCGCGCGCA 629  
Qy 121 GCTGCCCGCGGAGATGCTGTCGCGGAGGCGGCGAGCGGCGCGCGGCGGAGCTGCGG 180  
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Qy 181 CGCGCGCAGCTGCGCAAGTGGCGAGTGTGAGCTGGACCGAGCTGCTCAGCAGCGCTC 240  
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Qy 301 GCGGGAGTGGACCGCGCTTCCAGCGCTGTCGCGGTCGCGCGCGCGCGCGAGCGCGAG 360  
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Qy 481 CCCCGCGCTGTGAGATGAGAAATAAGAACTCTCAAAGSGTTGCAACAAGATGGATGAT 540  
Db 960 CCCTCGGTGAGAGATGAGAAATAAGAACTCTCAAAGSGTTGCAACAAGATGGATGAT 1019  
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3958 AATTACATCTTCTCAGAGAGAGAGTAGTAGAGCACTTGGAGAGCTTGGAGAGAGATAAG 4017  
4410 AATTACATCTTCTCAGAGAGAGAGTAGTAGAGCACTTGGAGAGCTTGGAGAGAGATAAG 4469  
4018 TATGAGGCTTTCAAAGATCAGTAGTTATTAACATCACTGAACAGATTCTCGTGGCCTT 4077  
4470 TATGAGGCTTTCAAAGATCAGTAGTTATTAACATCACTGAACAGATTCTCGTGGCCTT 4529  
4078 TCGTATCTCCATGAAGAACCAATCATTACAGAGATGTCAAGGTCCTCAATTTGCTTAAT 4137  
4530 TCGTATCTCCATGAAGAACCAATCATTACAGAGATGTCAAGGTCCTCAATTTGCTTAAT 4589  
4138 GACAGCACTGCTCAGAGACTTAAGATTTGCAATTTTGGAGCTGCGACCCAGGTTGGCATCA 4197  
4590 GACAGCACTGCTCAGAGACTTAAGATTTGCAATTTTGGAGCTGCGACCCAGGTTGGCATCC 4649  
4198 AAAGAACTGCTCAGAGAGAGTTTACAGGACATTTACTGGGACATTTGCATTTATGGCA 4257  
4650 AAAGAACTGCTCAGAGAGAGTTTACAGGACATTTACTGGGACATTTGCATTTATGGCG 4709

4258 CTTGAGGTACTTAAGAGGTCAACAGTATGGAAGAGCTGTGATGATGAGTGTGGCTGT 4317  
4710 CTTGAGGTACTTAAGAGGTCAACAGTATGGAAGAGCTGTGATGATGAGTGTGGCTGT 4769  
4318 GCTATTATAGAATGGCTTTGTGAAAAACACCATGGAATGCAAAAAACACTCCAATCAT 4377  
4770 GCAATTAAGAATGGCTTTGTGAAAAACACCATGGAATGCAAAAAACACTCCAATCAT 4829  
4378 CTTGCTTTGATATTTAAGATTGCTAGTGAATGCTACTGCTCCATGCTCCATGCTCCATTTG 4437  
4830 CTTGCTTTGATATTTAAGATTGCTAGTGAATGCTACTGCTCCATGCTCCATGCTCCATTTG 4889  
4438 TCTCCTGGTTTACGAGATGTGCTCTTCTGTTTGTAGAACTTCAACCTCAGACAGACCT 4497  
4890 TCCCGGGCTCGGAGACGTGCTCTGCGCTGTTTGAACCTTCAACCTCAGACAGACCT 4949  
4498 CCAATCAAGAGAGCTACTGAAGCATCCAGTCTTTTCTGCTACTGATGCTAGGCAATTTATG 4557  
4950 CCGTCAAGAGAGCTACTGAAGCATCCGCTCTTCCGTACCAATGCTAGTCAACT 5003  
4558 ATCAACTACAGTAGAACAAGGATGCTCAACAAGAGAAAAAACTTGTGGGAAACACAT 4617  
5004 -----GCTCAGGTTGCCAACAG-GAAGAAAACTCGCGGAGCCACCT 5048  
4618 TGATATTCTACTGGCCATGATGCCACTGAACAGCTATGAACAGGCACTGGGGAACCT 4677  
5049 TGATAGTCTGCTGGCC-TCATACCACTGACCAG----AAGAGGGGCGCAGTGGGAGCCCG 5103  
4678 TACTAAGTATGATGATGACAAATCATGATCTGCTACCTAAGCTCAGTATGCAAAAGCCCA 4737  
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4738 -AACTAGTCAGAAACTG 4754  
5163 CAACCTCGTCAGGAGCTG 5180

RESULT 8  
US-09-858-754-13  
; Sequence 13, Application US/09858754  
; Patent No. US20020055130A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, Gary L.  
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS  
; FILE REFERENCE: CFI-042  
; CURRENT APPLICATION NUMBER: US/09/858,754  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/023,130  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/039,740  
; PRIOR FILING DATE: 1997-02-14  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 5253  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (15)..(4493)  
US-09-858-754-13

Query Match 65.1%; Score 3417; DB 9; Length 5253;  
Best Local Similarity 83.5%; Pred. No. 0;  
Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;  
  
QY 1 GAGAAATGGCGCGCGCGGGAATCGCGCTCTGCTGGGATTCGCCGCGCCAGG 60  
DB 9 GAGAAATGGCGCGCGCGGCGATCGCGCTCTGCTGGGATTCGCCGCGCCAGG 68  
QY 61 GCTACGAGCCCTGAGGAGCGCGCGC-----GGAGGAGCCCTCAAGCGAGCAGC 111









Db	2259	GAAC	TGCTGGGTCGGCTCTGTCTTATACAGAGTTGCTGTTGGAAATTTCCCTGCTGAATTC	2316
Qy	2323	TATCCT	CATATTTGTGCTAGTACTGATGTTTTCACAGCTGAGCCTGTTGAAATCAGGTATTAAG	2382
Db	2319	TATCCTCT	CATATTTGTGCTAGTACTGATGCTCTCACAGCTGAGCCTGTTGAAATCAGGTACAAG	2378
Qy	2383	AAGCTGCT	CTCCCTCTTAACTTTTGCTTTGCACTCCATTTGCAATTTCCCACTCAATGGTT	2442
Db	2379	AAGCTGCT	CTCCCTCTTAACTTTTGCTTTGCAATTTCCCACTCGATGGTT	2438
Qy	2443	GGCAAA	CTTTCCAGAAAGGATCTACTTTGAGTTCTGCAAGAAATGGTTACTTACAGTACCCCAAT	2502
Db	2439	GGCAAGCT	CTCTCGAGAGGATATCTGAGCTCTGCCAGGATGGTGAACCGACGTGCCCGCT	2498
Qy	2503	GTGTTTTT	CAAACTGTTAGAAATGCTGAGTGTTCAGTTCCACTTCACCTTCAACCAAGATG	2562
Db	2499	GTGTTTTT	CCAGCTGTGAACCACTGTTAATGCTTTGCGCTCCACCCACTTCAACCAAGATG	2558
Qy	2563	CGTCCGCG	TTTGATGCTTATGCAATGAGGTGGAAATTTGCCAAGCCATTCAGTTGGGC	2622
Db	2559	CGCGCG	CTGATGCTATCGCGATGAGGTAGAAATTCGCGAGGTCTATCCAGCTGGGT	2618
Qy	2623	GTAGAGAC	CACTTTTGATGGTGTCAAACAGGACAGCTTCTTCAGAGCATCTGTTCCCAACAAC	2682
Db	2619	GTGGAGAC	CACTGTGATGGCATCAGGAAG---CTTACAGGCGGTGSCCCCAACCCAGC	2675
Qy	2683	TATCTG	GAAAACCAACAGAGAACAGTTCCCTCGAGTGCAACAGTCCATTTAGAGAAAACTGGA	2742
Db	2676	TGTC	-----AGAAAAAGCTCCCTTGAGCACACAGTCCATAGAGAGAAAACTGGA	2726
Qy	2743	AAAGGAT	TATGCTACAAAATTTAGTGGCCAGTTCTAGAGGACATTTCTGAGACACTGGCC	2802
Db	2727	AAAGGACT	TAAGTGTACGAGACTGAGTGGCAGCTCGGAGAGACATTTCTGACACTGGCC	2786
Qy	2803	AGCATTT	CAGTAGACCTTCTAGTTCAAACAACAACAACAACAACAACAACAACAACAACAACAACA	2862
Db	2787	GGCGTCT	CTCTGAGACTTCCAGCT-----CAACAACAACAACAACAACAACAACAACAACAACA	2831
Qy	2863	AAGCCAA	TGGTTCAAACAAGGAGACCCCAACAGTCACTGTTTGAACCTCTCCTCTTAA	2922
Db	2832	AAGCCAG	CGGTTCAAACAAGGAGACCCCAACAGTCACTGTTTGAACCTCTCCTCTCTG	2891
Qy	2923	TCTCAT	CATTTCCCAATTAATGTTTCCAGCCTTGTCAACCCCTCTCTCTTTACCCCATCT	2982
Db	2892	TC---	CTATGCTCAATTAATGTTTCCAGCACCATCAGCCCTTGTCTCTGCCCCGTCT	2948
Qy	2983	GTACCA	GCTGGCATGCAACAGATGCTCTTAAGCATAGACTTCAGGGAATTCATTCCTCTGC	3042
Db	2949	GTCC-----	-----CAGATATTTCTAAGCACAGACCCCAAGGCAATTTGTTCCCTGC	2993
Qy	3043	AGATAC	CTTCTGATCTCCTCAAAACACAGCGCAAGTTTCTCTACAAATTTCCACAGAAAC	3102
Db	2994	AAAATAC	CTTCCGCAATCTCTTCAGACAAGGCAAGTTCTCTCTACAAATTTCCAGAGAAC	3053
Qy	3103	TGTCCT	GTAAAAACAAGACTCAGATAAATTTTCCCACTGTTTACTAGTGAAGACCCCTTG	3162
Db	3054	TGCTCT	GTAAACCCGAGACTCAGACAGCTCTCCCACTGTTCTCACTAGTCAAGAACCCCA	3113
Qy	3163	CCCTCC	AGTACATACACAGGCCCAAGGCCATCTAGACTCAACCCAGGTAATACAAAGTAAA	3222
Db	3114	CCCTCC	AGTAAATACACAGGCCCAAGGCCATCCCAACCGTTTCGGGCACTTCAAGCAAA	3173
Qy	3223	CAGGAGAT	CCCTCAAAAAATAGCATGACACTTTGATCTGAAACAGTAGTTTCCAAATGTGAT	3282
Db	3174	CTAGGG	AGCCCAAAAAGTAGCATGACACTTGATCTGGGCAGTGTCTCCAGGTGTGAC	3233
Qy	3283	GCAGCT	TTTGGCTGTAGCAGCAATAGTAGTAATGCTGTTATATCCAGTGCAGACAGTG	3342
Db	3234	GCAGCT	TTTGGCGGGGCAACAGTGGCAACCGCGTCAATCCAGCCAGCAGACAGTG	3293
Qy	3343	TTCA	CCCCCAGTAGAGGAAAAATGCAAGTTAGATGTCAATACAGAGCTCAATCCAGTATT	3402
Db	3294	TTCA	CGCCGTTGAGGACAAGTGACGGTTAGATGTGAACCAACGAGCTCAATCCAGCATC	3353

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4434	Db	CCTCAGGACCGGCGCTCCGTCACAGAGAGTGTCTGAAACATCCGGTCTTCGGTACCAACGTGG	4493
4543	QY	TAGCCATTTATCCAGATCAACTACAGTAGAAGACAGGATGCTCAAAGAGAGAAAAAAACT	4602
4494	Db	TAGTTAAATTTTCAGATCAGCTCTTAATGGAGACAGGATATGCAACGGGAGAGAGAAAG	4553
4603	QY	TG-----TGGGGGAACACATTTGATTTCTACTGGCCATGATGCCACTGAACAGCTATGAAC	4658
4554	Db	AGAACTTGTGGGCGACCATGCCGCTAAACCGCAGCCCTCAGCGCACTGAAACAGCCAGAAAC	4613
4659	QY	GAGCCAGTGGGGAACCCCTTAAGTAAGTATGTGATGACAAATCATGATCTGTACTTAAG	4718
4614	Db	GGGGCCAGCGGGGAA--CCGTACTAGCATGTGATTTGACAAATCATGACCTGTACCTAAG	4672
4719	QY	CTCAGTATGCA--AAGSCCCAAACTGTGCAGAAACTGTAAACTGTGCGCTTTTCAAGAACT	4777
4673	Db	CTCGATATGAGACATCTACAGTCTGTGAGGAACTGACACCGTGCCTTTTCACAGGACT	4732
4778	QY	GGCCCTAGGTGAACAGGAAAAAATGAAGTTTGATGACTTAAATTGCGAAGCATTAATTT	4837
4733	Db	GGCTCTGGGGGACCAAGGAGGCGATGGAGTTTTCATGACTTAAAGAACAGAAAGCATAAAT	4792
4838	QY	TAATTTTTTGGAGCACTTTTTCAGAA	4864
4793	Db	TA--TTTTTTGGAGCACTTTTTCAGCTA	4817

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RESULT 10
US-10-000-864-1
; Sequence 1, Application US/10000864
; Publication No. US20020146798A1
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; GENERAL INFORMATION:
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
;
; FILE REFERENCE: CPI-085CEPPC
; CURRENT APPLICATION NUMBER: US/10/000,864
; CURRENT FILING DATE: 2001-10-31
; EARLIER APPLICATION NUMBER: 09/423,890
; EARLIER FILING DATE: 2000-06-03
; EARLIER APPLICATION NUMBER: PCT/US99/05556
; EARLIER FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: USSN 60/078,153
; EARLIER FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: USSN 60/099,165
; EARLIER FILING DATE: 1998-09-04
;
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 1
;
; LENGTH: 3911
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(3908)
;
US-10-000-864-1

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	Query Match	62.7%	Score 3286.4	DB 14	Length 3911	
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DB	1	CGGCTCGAAGCACCAGTGGTTGGAAGAGAAATAGCGAGGGCTCTGGTGGTAAAC	60			
QY	650	CAATCCCAAGTTAAAGGAGATGGATCTGAATCAATCACTTAGCAGCTGAGTCTCCAGGAG	709			
DB	61	CAATCCCAAGTTAAAGGAGATGGATCTGAATCACTTAGCAGCTGAGTCTCCAGGAG	120			
QY	710	AGGTCAGGCAAGTCGGGCTTCACAGCTTCCAAAGGCGGAGTCTCTTCTCTGGCA	769			

QY	3403	GAGGACCTCTTGAGGCATCTATGCCTTCAAGTGATACAACAGTAACTTTTAACTCAGAA	3462
DB	3354	GAGGACCTCTTGAGAGCATCCATGCCTTCAAGTGACGACGATCACTTTCAGTCCGAA	3413
QY	3463	GTGTGTCCTGCTCTCCTGAAAGGCTGAAATATGATATACCTCAAGATGATGTGAAT	3522
DB	3414	GTGCGGCTCTCTCTCCGMAAAGCCGAAATACGACACCTCAAGAGCAGCGTCAAT	3473
QY	3523	CATANTCAAAAGTGCARAGAGAGATGAAGCTGAAGAGAGAAAGCTTTTAGCAATTGCC	3582
DB	3474	CATAATCAAAAGTGCARAGAAAGATGGAAGCTGAAAGAGGAGGCTTTTAGCGATCGCC	3533
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DB	3534	ATGGCGATGTCAAGCGTCTCAGGATGCCCTCCCATCGTCCCTCAGCTCAGGTGGAAAT	3593
QY	3643	GGAGAGATATCATCATATTATCAACAGAGATACACCAGAGACTCTACACAGGACATACC	3702
DB	3594	GGAGAGATATATTATCATCATTCATCAGCAGGACACACCGAAATCTCTTCAGGACATACC	3653
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DB	3654	GCGAAACAGCCTTACAGAGAAGACGCTGAGTGGCTGAAAGGCCAGCAGATAGGCCCTGA	3713
QY	3763	GCATTTCTCTCTGTTTATCAGGCTCAAGATGTGGGAACCTGGAACCTTTAATGGCTCTTAA	3822
DB	3714	GCATTTCTCTCTGTTTACCAGACAGGATGTGGGACTTGGGACCTTTAATGGCTCTGAA	3773
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DB	3774	CAGTGACGTACGTCAGAAACACATCCTCCGAGCAGGAGGAGTGGTGAAGCGTTGAGG	3833
QY	3883	GAGAGATAGATGATGGCCATCTGAATCATCCAAACATCATATTAGGATGTTGGAGCC	3942
DB	3834	GAGAGATCCGGATGATGGGTCACTTACCCTAACCATCCAAACATCATCCGATGCTGGGGCC	3893
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DB	3894	ACGTGCGAGAAGAGCAACTACAACCTCTTCATTGATGGATGGCGGAGGATCTGTGGCT	3953
QY	4003	CATTGCTGAGTAAATATGAGCGCTTCAAGATCAGTATGTTATTAACTACACTGAACAG	4062
DB	3954	CACCTTTGATGATAACGGAGCTTTCAAGAGTCACTGCTCATTAATCTACACTGAGCAG	4013
QY	4063	TTACTCCGTGGCCCTTTCTGATCTCCATGAAAAACCAATCATTCACAGAGATGCAAGGT	4122
DB	4014	TTACTCGTGGCCCTTTCTCTCTCCACGAAACAGATCATTCACAGAGACGCTCAAGGT	4073
QY	4123	GCCAAATTGCTAATTGACAGCATCTGGTCAGAGACTAAGATTCAGATTTGGAGCTGCA	4182
DB	4074	GCCAACTGCTCATGTGACAGCACCGGTCAGAGGCTGAAATTCGAGACNTTGGAGCTGCT	4133
QY	4183	GCCAGGTGGCATCAAAAGGAACCTGGTCGAGGAGAGTTTCAGGACAAATPACTGGGGACA	4242
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QY	4243	ATTGCATTTATGGCACTGAGGTACTAAGAGGTCAACAGTATGGAAGAGCTGTGATGTA	4302
DB	4194	ATTGCATTCATGGGCGCTTGAGTCTTAAGAGGTCGCGATATGGTAGGAGCTGTGATGTA	4253
QY	4303	TGGAGTGTGGCTGTGCTATTATAGAAATGGCTTTGTCAAAACCAACCATGGAATGAGAA	4362
DB	4254	TGGAGTGTGGCTGCGCCATTATAGAAATGGCTTTGTCAAAACCAACCTTGGAAATGAGAA	4313
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DB	4374	ATCCCTTTCACATCTGCTTTCGATATTAAAGATTCCTAGTGCAACTACTGCTCCATCG	4433



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Db 181 ACTCCCATCAGGTGGCAGACAGTGAATCAGAACTCTCAGGAGTAAAGAGAAAGAGTTT 240  
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Qy 890 GCTTCTACCATATAGCCCTCAGAGAAACAAACCGCGGTGTTTAAACAAAGTGAATGGGGCCA 949  
Db 301 GCTTCTACCATATAGCCCTCAGAGAAACAAACCGCGGTGTTTAAACAAAGTGAATGGGGCCA 360  
Qy 950 GACTGTACTTACTCAGCAGATAGGCGCTAACTCTTCTCTGANTGGAGGAGACAGCCAG 1009  
Db 361 GACTGTACTTACTCAGCAGATAGGCGCTAACTCTTCTCTGANTGGAGGAGACAGCCAG 420  
Qy 1010 ACAATAATACGGGTGTTTATTTGGCCCTCAGAACTGCAGCTGTGCAGTGGRAACTTCT 1069  
Db 421 ACAATAATACGGGTGTTTATTTGGCCCTCAGAACTGCAGCTGTGCAGTGGRAACTTCT 480  
Qy 1070 GTATTCACTCTGTAATTTGTGATGCTCCGGGTGTTTCACTAGAACTTTCAGACCCAAATGT 1129  
Db 481 GTATTCACTCTGTAATTTGTGATGCTCCGGGTGTTTCACTAGAACTTTCAGACCCAAATGT 540  
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Db 541 TATGGAGAAACCTTTAAGAACTTTGAGGTTGAGGTTTCTCCAGAAATATCACAGTA 600  
Qy 1190 GCGGTAGTCAAGGATCAAGCTCCATCTCGTAAACACCATCCAGAAAGTTTGTTCACGCA 1249  
Db 601 GCGGTAGTCAAGGATCAAGCTCCATCTCGTAAACACCATCCAGAAAGTTTGTTCACGCA 660  
Qy 1250 TGTCAAACTTCATACATGTCATCTAGTACTTCTACGTTCTAGTTCAGAAACAGCA 1309  
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Db 721 TAAAGATGAAGAGAAACAGATGTCCTATTGCTTGTGGGCATGCTTGATGAAGAAA 780  
Qy 1370 GTCTTACAGTGTGAAGACGCTCGAGAAACAGCTGCAACACACTGCATGTCATTT 1429  
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Qy 1430 GGGCAGACAGTGTGAAGAAATAGAAACCTTTAATATGTCCTTTGTAGATCTAAGT 1489  
Db 841 GGGCAGACAGTGTGAAGAAATAGAAACCTTTAATATGTCCTTTGTAGATCTAAGT 900  
Qy 1490 GGAGATCTCATGATTTCTACGCCACGAGTGTCAAGTCTGTGGANTCCCTTCTTCCC 1549  
Db 901 GGAGATCTCATGATTTCTACGCCACGAGTGTCAAGTCTGTGGANTCCCTTCTTCCC 960  
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Qy 1670 ATTTAGCTAGCCATGGATTCAGGTGTTTGAATGGAACTCGTTGGCTGCTTATTTCTTA 1729  
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Qy 1850 GTGGGGAGCCACCAAGTGGGTCTTCCAGAGCCAGTATCTCAGGAGATGTGTGGAGGAT 1909  
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Qy 2150 GAGAGTTGGCAGTTGGCAGAGAAATCTTAAAGCTGGATCCATTTGGTATTTGGTGTG 2209  
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Qy 2330 ATATTGTCAAGTCTGATGTTTCAAGCTGAGCTGTTGAAATCAGGTATTAAGAACTGC 2389  
Db 1741 ATATTGTCAAGTCTGATGTTTCAAGCTGAGCTGTTGAAATCAGGTATTAAGAACTGC 1800  
Qy 2390 TGTCCCTCTTAACTTTGTTTGGCTTCAATGATTAATTTCCCACTCAATGTTGGGCAAC 2449  
Db 1801 TGTCCCTCTTAACTTTGTTTGGCTTCAATGATTAATTTCCCACTCAATGTTGGGCAAC 1860  
Qy 2450 TTTCCAGAGGATCTACTTGGTCTGCAAGATGTTTACTACAGTACCCCATGTTGTTT 2509  
Db 1861 TCTCTCGAGGATATATCTGAGCTCTGCCAGATGTTGACCGCAGTGCCTGCTGTTT 1920  
Qy 2510 CAAACCTGTTAGAAATGCTGAGTGTTCAGTTCCTCACTCACTTCAAGAGTGGTGC 2569  
Db 1921 CCAAGCTGGTAAACCATGCTTAATGCTTCTGGCTCCACCACTTCCACAGGATCGCGCGC 1980  
Qy 2570 GTTTGATGGCTATTGAGATGAGGTGGAATTCGCCAGCCATCCAGTTGGGCGTAGAAG 2629  
Db 1981 GTCTGATGGCTATTGCGGATGAGGTAGAAATTCGCCAGGTCTCCAGCTGGGTGGAGG 2040  
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Qy 2690 AAACCCAGAGAACAGTTCCTCTGAGTGCAGCTCCATTTAGGAAACTGGAAGAGAT 2749  
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Qy 2750 TATGTGCTCAAAATTTGAGTGCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGCATTTT 2809  
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Qy 2810 CAGTAGACCTTCTGATTTAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA 2869  
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1086	DB	TGAGGGCTCAGGATCTATTTTAAATATTCATTTCTTCCATTTCCATATATGTGATCAC	1145
4935	QY	AAGCAGGGGGTCTCGCAATTCGGTCCAAATTTTGTGCATCGGCTATAAATCAGTATCT	4994
1146	DB	AAGCAGGGGGTCTCGCAATTCGGTCCAAATTTTGTGCATCGGCTATAAATCAGTATCT	1205
4995	QY	GCCTCTTTTAGGTCAGAGTAGTGCATCAGTAGCAATACATACATATATTTTAAAGTTG	5054
1206	DB	GCCTCTTTTAGGTCAGAGTAGTGCATCAGTAGCAATACATACATATATTTTAAAGTTG	1265
5055	QY	ATACCTCTTTAAGCCACAGTGCACCTTTATTTTCTTAATACCGGGCAGTTGTGGCT	5114
1266	DB	ATACCTCTTTAAGCCACAGTGCACCTTTATTTTCTTAATACCGGGCAGTTGTGGCT	1325
5115	QY	CATTGTGCATTTTACTGTTGGCCCATTCATTTCGTTTTTGGAAATATGTTTTGTATTT	5174
1326	DB	CATTGTGCATTTTACTGTTGGCCCATTCATTTCGTTTTTGGAAATATGTTTTGTATTT	1385
5175	QY	TCATGTTTTATTACATTCATTTTTGTTTTTATTCAGGGAAGCTGATCTTTTTTCAACCC	5234
1386	DB	TCATGTTTTATTACATTCATTTTTGTTTTTATTCAGGGAAGCTGATCTTTTTTCAACCA	1445
5235	QY	AAAAAATAA 5244	
1446	DB	GAATAAATAA 1455	

## RESULT 13

US-09-796-692-6957/c  
; Sequence 6957, Application US/09796692  
; Publication No. US20020198362A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF  
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES  
; FILE REFERENCE: 2077.001200  
; CURRENT APPLICATION NUMBER: US/09/796,692  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: 60/223,378  
; PRIOR FILING DATE: 2000-08-07

```

; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6957
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (528)
; OTHER INFORMATION: n=A,T,C or G
US-09-796-692-6957

Query Match          10.5%; Score 549; DB 9; Length 550;
Best Local Similarity 99.8%; Pred. No. 1.9e-138;
Matches 549; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2251 AACAAATTGGCAAGAACCTCTTGCCGCCCTTTGCTTTATAGATAGACTGTGTGTGGAAATTT 2310
Db 550 AACAAATTGGCAAGAACCTCTTGCCGCCCTTTGCTTTATAGATAGACTGTGTGTGGAAATTT 491
QY 2311 CCTGCTGAATTTTATCCTCATATATGTCAGTACTGATGTTTCAAGCTGAGCCTGTGGAA 2370
Db 490 CCTGCTGAATTTTATCCTCATATATGTCAGTACTGATGTTTCAAGCTGAGCCTGTGGAA 431
QY 2371 ATCAGGTATAGAAGCTGCTGCCCTTAACTTTGCTTTGAGTCCCATTGATAATTC 2430
Db 430 ATCAGGTATAGAAGCTGCTGCCCTTAACTTTGCTTTGAGTCCCATTGATAATTC 371
QY 2431 CACTCAATGTTGGCAAACTTTTCAGAAAGATCTACTGTAGTCTGCGAAGATGGTTACT 2490
Db 370 CACTCAATGTTGGCAAACTTTTCAGAAAGATCTACTGTAGTCTGCGAAGATGGTTACT 311
QY 2491 ACAGTACCCATGTGTTTTCAAAACCTGTTAGAAATGCTGAGTGTTCAGTTCACACTCAC 2550
Db 310 ACAGTACCCATGTGTTTTCAAAACCTGTTAGAAATGCTGAGTGTTCAGTTCACACTCAC 251
QY 2551 TTCACCAAGATGCGTCGCCGTTTGATGGCTATTGCGATGAGGTGGAATTCGCCAAGCC 2610
Db 250 TTCACCAAGATGCGTCGCCGTTTGATGGCTATTGCGATGAGGTGGAATTCGCCAAGCC 191
QY 2611 ATCCAGTTGGCGTGAAGACACTTTTGGATGGTTCACAGACAGACTCTTTCGAGGCACTC 2670
Db 190 ATCCAGTTGGCGTGAAGACACTTTTGGATGGTTCACAGACAGACTCTTTCGAGGCACTC 131
QY 2671 GTTCCCACACTATCTGGAAACACAGAGAAACAGTTCCTCCCTGAGTGCACAGTCCCAATTA 2730
Db 130 GTTCCCACACTATCTGGAAACACAGAGAAACAGTTCCTCCCTGAGTGCACAGTCCCAATTA 71
QY 2731 GAGAAAACGTGAAAAGGATTTATGTGCTACAAAATTTGAGTCCAGTTCAGAGGACATTTCT 2790
Db 70 GAGAAAACGTGAAAAGGATTTATGTGCTACAAAATTTGAGTCCAGTTCAGAGGACATTTCT 11
QY 2791 GAGAGACTGG 2800
Db 10 GAGAGACTGG 1

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## RESULT 14

US-10-040-862-6957/c  
 ; Sequence 6957, Application US/10040862  
 ; Publication No. US20030078396A1  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Mannion, Jane  
 ; APPLICANT: Retter, Marc  
 ; APPLICANT: Corixa Corporation  
 ;  
 ; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy,  
 ; of Hematological Malignancies  
 ;  
 ; FILE REFERENCE: 014058-013520US  
 ;  
 ; CURRENT APPLICATION NUMBER: US/10/040,862  
 ;  
 ; CURRENT FILING DATE: 2001-11-06  
 ;  
 ; PRIORITY APPLICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: US 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: US 60/223,416  
PRIOR FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: US 60/223,378  
PRIOR FILING DATE: 2000-08-07  
PRIOR APPLICATION NUMBER: US 08/796,692  
PRIOR FILING DATE: 2001-03-01  
NUMBER OF SEQ ID NOS: 10467  
SOFTWARE: Fast-SEQ for Windows Version 3.0  
SEQ ID NO 6957  
LENGTH: 550  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (528)  
OTHER INFORMATION: n=A,T,C or G  
US-10-040-862-6957

Query Match 10.5%; Score 549; DB 15; Length 550;

Best Local Similarity 99.8%; Pred. No. 1.9e-138; Indels 0; Gaps 0;  
Matches 549; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2251 AACAAATGGCAAGAACTCTTGGCGCTTTGCTTATAGATAGACTGTTGGAAATTT 2310  
550 AACAAATGGCAAGAACTCTTGGCGCTTTGCTTATAGATAGACTGTTGGAAATTT 491  
2311 CTGCTGAAATTTATCTCTATATTCAGTACTGTTTACAGAGCTGAGCTGTTGAA 2370  
490 CTGCTGAAATTTATCTCTATATTCAGTACTGTTTACAGAGCTGAGCTGTTGAA 431  
2371 ATCAGGTATAAGAGCTGCTGCTCTTAACTTTGCTTTCAGTCCATTGATATTC 2430  
430 ATCAGGTATAAGAGCTGCTGCTCTTAACTTTGCTTTCAGTCCATTGATATTC 371  
2431 CACTCAATGGTTGGCAAACTTTCCAGAGGATCTACTGATTTCCAGAGATGTTACT 2490  
370 CACTCAATGGTTGGCAAACTTTCCAGAGGATCTACTGATTTCCAGAGATGTTACT 311  
2491 ACAGTACCCCATGCTGTTTTCAAACTGTTAGAAATGCTGAGTGTTCAGTTCACCTCAC 2550  
310 ACAGTACCCCATGCTGTTTTCAAACTGTTAGAAATGCTGAGTGTTCAGTTCACCTCAC 251  
2551 TTCACAGAGATCGTGGCGCTTTGATGCTATTCAGATAGGTGGAAATTCGAGGCC 2610  
250 TTCACAGAGATCGTGGCGCTTTGATGCTATTCAGATAGGTGGAAATTCGAGGCC 191  
2611 ATCCAGTTGGGCGTAGAGACACTTTGGATGTTCAACAGGACAGCTTCTTCAGGCACT 2670  
190 ATCCAGTTGGGCGTAGAGACACTTTGGATGTTCAACAGGACAGCTTCTTCAGGCACT 131  
2671 GTTCCCAACAACTATCTGAAACCCACAGAGAACAGTTCCTCCCTGAGTGCAGCTCATTTA 2730  
130 GTTCCCAACAACTATCTGAAACCCACAGAGAACAGTTCCTCCCTGAGTGCAGCTCATTTA 71

2731 GAGAAACTGAAAGGATTTATGCTCAAAATGAGTGCCAGTTTCAGAGACATTTCT 2790  
70 GAGAAACTGAAAGGATTTATGCTCAAAATGAGTGCCAGTTTCAGAGACATTTCT 11  
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10 GAGAGACTGG 1

## RESULT 15

US-10-057-475B-6957/c  
Sequence 6957, Application US/10057475B  
Publication No. US20040002068A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Algate, Paul A.  
APPLICANT: Mannion, Jane  
APPLICANT: Clapper, Jonathan David  
APPLICANT: Wang, Aijun  
APPLICANT: Ordenez, Nadia  
APPLICANT: Carter, Lauren  
APPLICANT: McNeill, Patricia Dianne  
APPLICANT: Corixa Corporation  
TITLE OF INVENTION: Hematological Malignancies  
FILE REFERENCE: 014058-014402US  
CURRENT APPLICATION NUMBER: US/10/057,475B  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: US 60/186,126  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: US 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 10973

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 6957

LENGTH: 550

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)...(550)

OTHER INFORMATION: n = g, a, c or t

US-10-057-475B-6957

Query Match 10.5%; Score 549; DB 16; Length 550;

Best Local Similarity 99.8%; Pred. No. 1.9e-138;

Matches 549; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2251 AACAAATGGCAAGAACTCTTGGCGCTTTGCTTATAGATAGACTGTTGGAAATTT 2310

550 AACAAATGGCAAGAACTCTTGGCGCTTTGCTTATAGATAGACTGTTGGAAATTT 491

2311 CTGCTGAAATTTATCTCTATATTCAGTACTGTTTCAAGCTGAGCTGTTGAA 2370

490 CTGCTGAAATTTATCTCTATATTCAGTACTGTTTCAAGCTGAGCTGTTGAA 431







source	1..5245	Query Match	100.0%	Score 5245;	DB 6;	Length 5245;	
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QY	1	GAGAAATGGCGCGCGCGCGGAGATCGCGCTCGTCTCGGATTC	CGCGCGCGCGG	60			
Db	1	GAGAAATGGCGCGCGCGCGGAGATCGCGCTCGTCTCGGATTC	CGCGCGCGCGG	60			
QY	61	GCTACGAGCCCTGAGGCAAGCGCGCGGAGAGCCCTCAAGGCGAGAGCGCGCGCGG	120				
Db	61	GCTACGAGCCCTGAGGCAAGCGCGCGGAGAGCCCTCAAGGCGAGAGCGCGCGCGG	120				
QY	121	GCTGCCGGGAGTCTCTCGGAGAGCGGAGCGGCGGCGGCGGAGCGGCGGATCGCGG	180				
Db	121	GCTGCCGGGAGTCTCTCGGAGAGCGGAGCGGCGGCGGCGGAGCGGCGGATCGCGG	180				
QY	181	CGCGCGAGCTGCGCAAGTGGAGTGGAGCTGGACCAAGCTGCTGAGCAGCGCGTC	240				
Db	181	CGCGCGAGCTGCGCAAGTGGAGTGGAGCTGGACCAAGCTGCTGAGCAGCGCGTC	240				
QY	241	TTCTTGGCGCTCACCGCGGCTCTCTCGATTCCTCCGCTCGCGGAGCGCGGAGCGCA	300				
Db	241	TTCTTGGCGCTCACCGCGGCTCTCTCGATTCCTCCGCTCGCGGAGCGCGGAGCGCA	300				
QY	301	GCGGGAGTGGACCGGCTTCCAGCTGTGGCGGTGCGCGCGCGCGCGCGGAGCGCGAGC	360				
Db	301	GCGGGAGTGGACCGGCTTCCAGCTGTGGCGGTGCGCGCGCGCGCGCGGAGCGCGAGC	360				
QY	361	CGCGCGCGCGCCACTTACCGAGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG	420				
Db	361	CGCGCGCGCGCCACTTACCGAGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG	420				
QY	421	GCAGCGCGCGAGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	480				
Db	421	GCAGCGCGCGAGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	480				
QY	481	CCGCGCGTGGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	540				
Db	481	CCGCGCGTGGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	540				
QY	541	CGTCCAGAGGACGATGATCAGGAGAACTGAAGCAACCTGTATGCCAGCTGGAG	600				
Db	541	CGTCCAGAGGACGATGATCAGGAGAACTGAAGCAACCTGTATGCCAGCTGGAG	600				
QY	601	CAGGAATGGTGAAGGAGAAATAGCGAGGCGCTGTGGTGAAGCAATCCAGTT	660				
Db	601	CAGGAATGGTGAAGGAGAAATAGCGAGGCGCTGTGGTGAAGCAATCCAGTT	660				
QY	661	AAAGGAGTGGATCTGAATGAATCACTTAGCAGCTGAGTCTCCAGAGAGAGTCCAGGCA	720				
Db	661	AAAGGAGTGGATCTGAATGAATCACTTAGCAGCTGAGTCTCCAGAGAGAGTCCAGGCA	720				
QY	721	AGTGGGCTTACAGCTTCAAGGCGCGAGGCTCTTCTCTCGGCACTCCCGCATCA	780				
Db	721	AGTGGGCTTACAGCTTCAAGGCGCGAGGCTCTTCTCTCGGCACTCCCGCATCA	780				
QY	781	GGTGGCAGCTGAATCAGAACTCTCAGGAGTGAAGGAGAAAGATTTCCCGAGTGC	840				
Db	781	GGTGGCAGCTGAATCAGAACTCTCAGGAGTGAAGGAGAAAGATTTCCCGAGTGC	840				
QY	841	TTTTCAGATGGAGATCAACACCGCGAGGCGCTTCAACAGATGGCTTCTCACA	900				
Db	841	TTTTCAGATGGAGATCAACACCGCGAGGCGCTTCAACAGATGGCTTCTCACA	900				
QY	901	TATAGCCCTGAGGAAACAAACCGCGCTGTAAACAAAGTATGGGCGCAGAGTACTTA	960				
Db	901	TATAGCCCTGAGGAAACAAACCGCGCTGTAAACAAAGTATGGGCGCAGAGTACTTA	960				

QY	961	CTCCAGAGATAGGCGCTTAACCTCTTCTGATGTGAGGAGAGCGCCAGACAATAATAC	1020				
Db	961	CTCCAGAGATAGGCGCTTAACCTCTTCTGATGTGAGGAGAGCGCCAGACAATAATAC	1020				
QY	1021	CGGGTGTATTGGGCGCTCAGAACTGCGAGCTGCGACGTGGAACTTCTGTATTCTATCTG	1080				
Db	1021	CGGGTGTATTGGGCGCTCAGAACTGCGAGCTGCGACGTGGAACTTCTGTATTCTATCTG	1080				
QY	1081	CTATTGTGATGCTCGGGTGTTCAACTAGAACCTTCAGACCCCAATGTATTGGAGAAA	1140				
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QY	1141	ACTTTAAAGAAATTTGAGGTTGAGAGTTGTTCCAGAAATATCAGTAGGCGTAGCTCA	1200				
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Db	1201	AGGATCAAAAGCTCCATCTCGTAACACCATCCAGAAAGTTGTTTTCACGATGTCAAATTC	1260				
QY	1261	CATACATTGTCATCATCTAGTACTTCTAGCTAGTTCAGAAACAGCATAAAGATGAA	1320				
Db	1261	CATACATTGTCATCATCTAGTACTTCTAGCTAGTTCAGAAACAGCATAAAGATGAA	1320				
QY	1321	GAGGAAACAGATGTCCTATTGCTTGTGGCATCTGTGATGAAGAAAGTCTTACAGTG	1380				
Db	1321	GAGGAAACAGATGTCCTATTGCTTGTGGCATCTGTGATGAAGAAAGTCTTACAGTG	1380				
QY	1381	TGTGAAGAGCGTGCAGGAGCAAGCTGCACCACTGCTCAATTTGGGCGAGAG	1440				
Db	1381	TGTGAAGAGCGTGCAGGAGCAAGCTGCACCACTGCTCAATTTGGGCGAGAG	1440				
QY	1441	TGTGAAGAAATAGAGAACCTTTAATATGTCCTTGTGATGATCAAGTGGAGATCTCAT	1500				
Db	1441	TGTGAAGAAATAGAGAACCTTTAATATGTCCTTGTGATGATCAAGTGGAGATCTCAT	1500				
QY	1501	GATTCTACAGCAAGTGTCAAGTCTGTGGATTCCTCTTCCCTTCTCCCTCAGAGTGCA	1560				
Db	1501	GATTCTACAGCAAGTGTCAAGTCTGTGGATTCCTCTTCCCTTCTCCCTCAGAGTGCA	1560				
QY	1561	CACGAGCAAAACCGTACAGCAGCAGCCTTTGGGTGGATCGAAGGAATCAAGAGAGCAAT	1620				
Db	1561	CACGAGCAAAACCGTACAGCAGCAGCCTTTGGGTGGATCGAAGGAATCAAGAGAGCAAT	1620				
QY	1621	TTTAACTTACTCATTTATGGAATCGAATAATCCCTCTGCTTCAAGATTTAGGTGAG	1680				
Db	1621	TTTAACTTACTCATTTATGGAATCGAATAATCCCTCTGCTTCAAGATTTAGGTGAG	1680				
QY	1681	CCATGGATTGAGGTTTGGAACTGGAATCGTGGCTGCTTATTTCTAGAAACTGGAAT	1740				
Db	1681	CCATGGATTGAGGTTTGGAACTGGAATCGTGGCTGCTTATTTCTAGAAACTGGAAT	1740				
QY	1741	GTGAGAGATGCGCTCAGGCGTCTTTCCATGATGTGAGTGGGCGCTGCTGTGGCA	1800				
Db	1741	GTGAGAGATGCGCTCAGGCGTCTTTCCATGATGTGAGTGGGCGCTGCTGTGGCA	1800				
QY	1801	AATGGGAGAGCACTGGAATCTTGGGGCAGCAGTGGAAAGCAGCCGAGTGGGGAGCC	1860				
Db	1801	AATGGGAGAGCACTGGAATCTTGGGGCAGCAGTGGAAAGCAGCCGAGTGGGGAGCC	1860				
QY	1861	ACCAAGTGGTCTTCCAGACCACTATCTCAGGAGATGTGGTGGAGCGATGCTGACGGTT	1920				
Db	1861	ACCAAGTGGTCTTCCAGACCACTATCTCAGGAGATGTGGTGGAGCGATGCTGACGGTT	1920				
QY	1921	CTGTCAATGCTGTGCTGACCCCTGCTCAAAAGTGTAGTCTGCTTTTAAAAACATTC	1980				
Db	1921	CTGTCAATGCTGTGCTGACCCCTGCTCAAAAGTGTAGTCTGCTTTTAAAAACATTC	1980				
QY	1981	AGAGCCATGCTGTATATCTCTTCCACAGTTTAGCGGAAAGATCAAACTTTCAGAGA	2040				
Db	1981	AGAGCCATGCTGTATATCTCTTCCACAGTTTAGCGGAAAGATCAAACTTTCAGAGA	2040				
QY	2041	CTTCTCCAGCCAGTTGTAGACACCATCTCTAGTCAATGTGACATGCCATATGCCGACA	2100				



QY	4261	GAGGTACTAAGAGGTCAACAGTATGGAAGAGCTGTGATGTATGAGGTGTGGCTGTGCT	4320
DB	4261	GAGGTACTAAGAGGTCAACAGTATGGAAGAGCTGTGATGTATGAGGTGTGGCTGTGCT	4320
QY	4321	ATTATAGAAATGCTTGTGCAGAAACCAACATGCAAGATGCAGAAAAACACTTCCAATCATCTT	4380
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QY	4381	GCCTTGATATTTAAGATGTGTAGTGGAACTACTGTCTCCATCGATCCCTTCACTTTGTCT	4440
DB	4381	GCCTTGATATTTAAGATGTGTAGTGGAACTACTGTCTCCATCGATCCCTTCACTTTGTCT	4440
QY	4441	CCTGGTTTACGAGATGTGGCTCTTCGTGTGTTAGAACTCTCAACCTCAGACAGACCTCCA	4500
DB	4441	CCTGGTTTACGAGATGTGGCTCTTCGTGTGTTAGAACTCTCAACCTCAGACAGACCTCCA	4500
QY	4501	TCAAGAGAGCTACTGAAGCATTCAGTCTTTTCGTACTACATGGTAGCCATTAATGCAGATC	4560
DB	4501	TCAAGAGAGCTACTGAAGCATTCAGTCTTTTCGTACTACATGGTAGCCATTAATGCAGATC	4560
QY	4561	AACTACAGTAGAAACAGAGATGCTCAAACAGAGAAAAAAAACCTTGTGGGAAACCAATTGA	4620
DB	4561	AACTACAGTAGAAACAGAGATGCTCAAACAGAGAAAAAAAACCTTGTGGGAAACCAATTGA	4620
QY	4621	TATTTCTACTGGCCATGATGCCACTGACAGCTATGACAGAGGCCAGTGGGGAAACCCCTTAC	4680
DB	4621	TATTTCTACTGGCCATGATGCCACTGACAGCTATGACAGAGGCCAGTGGGGAAACCCCTTAC	4680
QY	4681	CTAAGTATGTGATTGACAAATCATGATCTGTACTAAAGCTCAGTATGCAAAAAGCCCAAAC	4740
DB	4681	CTAAGTATGTGATTGACAAATCATGATCTGTACTAAAGCTCAGTATGCAAAAAGCCCAAAC	4740
QY	4741	TAGTGCAGAAACTGTAACTCTGCTTTCAAAGAACTGGCCCTAGGTGAAACAGAAAAACA	4800
DB	4741	TAGTGCAGAAACTGTAACTCTGCTTTCAAAGAACTGGCCCTAGGTGAAACAGAAAAACA	4800
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QY	4861	GCAATATTAGCGGCTGAGGGGCTCAGGATCTATTTTAATAATTTCAATTAATTTTCCATTT	4920
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QY	4921	CATATAGTATGATCAACAGAGGGGGTTCTGCAATTCGGTCAAAATTTTGTCTACTGGCTA	4980
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QY	4981	TAAATCAGTATCTGCCCTCTTTTAGGTACAGAGTATGCTATCAGTAGCAATACATACATAT	5040
DB	4981	TAAATCAGTATCTGCCCTCTTTTAGGTACAGAGTATGCTATCAGTAGCAATACATACATAT	5040
QY	5041	ATTTTAAAGTTGATCTCTTTATGACCCACAGTTGACCTTTATTTCTTAAATACCA	5100
DB	5041	ATTTTAAAGTTGATCTCTTTATGACCCACAGTTGACCTTTATTTCTTAAATACCA	5100
QY	5101	GGGCAGTTGTGGCTCATTTGTGCATTTTACTGTGGCCCAATCATTTCTTTTGGAAATT	5160
DB	5101	GGGCAGTTGTGGCTCATTTGTGCATTTTACTGTGGCCCAATCATTTCTTTTGGAAATT	5160
QY	5161	ATGGTTTGTATTTTTCATGTTTATTTATCATTTTGTGTTTATTCAGGGAAGCTGATC	5220
DB	5161	ATGGTTTGTATTTTTCATGTTTATTTATCATTTTGTGTTTATTCAGGGAAGCTGATC	5220
QY	5221	TTTTTTTTTCAAAACCAAAAAAAAAAAAAA	5245
DB	5221	TTTTTTTTTCAAAACCAAAAAAAAAAAAAA	5245

RESULT 2				
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LOCUS	AX780290	5238 bp	DNA	linear
				PAT 14-JUL-2003

Sequence 2447 from Patent WO03039443.

AX780290  
 AX780290.1 GI:32697284

Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1  
 Haerlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S.,  
 Dugas, M., Ellis, R., Brors, B. and Mergenthaler, S.  
 Novel genetic markers for leukemias  
 Patent: WO 03039443-A 2447 15-MAY-2003;  
 Deutsches Krebsforschungszentrum (DE);  
 Ludwig-Maximilians-Universität München (DE);  
 PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)

Location/Qualifiers  
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ORIGIN

Query Match 96.2%; Score 5043.6; DB 6; Length 5238;  
 Best Local Similarity 98.3%; Pred. No. 0;  
 Matches 5102; Conservative 0; Mismatches 79; Indels 8; Gaps 3

QY 65 CGAGCCCTGAGCAGCGCGCGCGAGGAGCCCTCAAGGCAGCAGCGCGCGGGCTG 124  
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## RESULT 5

AF042838 4693 bp mRNA linear PRI 18-DEC-1998  
LOCUS Homo sapiens MEK kinase 1 (MEK1) mRNA, partial cds.  
DEFINITION  
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VERSION AF042838.1 GI:2815887  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Xia, Y., Wu, Z., Su, B., Murray, B. and Karin, M.  
TITLE JNK1 organizes a MAP kinase module through specific and sequential interactions with upstream and downstream components mediated by its amino-terminal extension  
JOURNAL Genes Dev. 12 (21), 3369-3381 (1998)  
MEDLINE 99026111  
PUBMED 9808624  
REFERENCE  
AUTHORS Xia, Y., Su, B. and Karin, M.  
2 (bases 1 to 4693)

TITLE Direct submission  
 JOURNAL Submitted (13-JAN-1998) Pharmacology, University of California at San Diego, 9500 Gilman Drive, La Jolla, CA 92093, USA  
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DEFINITION U48596
VERSION U48596.1 GI:1354136
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SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 5180)
AUTHORS Xu,S., Robbins,D.J., Christerson,L.B., English,J.M., Vanderbilt,C.A. and Cobb,M.H.
TITLE Cloning of rat MEK kinase 1 cDNA reveals an endogenous membrane-associated 195-kDa protein with a large regulatory domain
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (11), 5291-5295 (1996)
MEDLINE 96224276
PubMed 8643568
REFERENCE 2 (bases 1 to 5180)
AUTHORS Cobb,M.H.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1996) Melanie H. Cobb, Department of Pharmacology, University of Texas Southwestern Medical Center at Dallas, 5323 Harry Hines Blvd., Dallas, TX 75235, USA
FEATURES
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gene
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TITLE	Human MEKK proteins, corresponding nucleic acid molecules, and uses therefor
JOURNAL	US 6312934-A 7 06-NOV-2001;
FEATURES	Location/Qualifiers
source	1. 5253
	/organism="unknown"
	/mol types="unassigned DNA"

## ORIGIN

Query Match 65.1%; Score 3417; DB 6; Length 5253;  
Best Local Similarity 83.5%; Pred. No. 0;  
Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;

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Qy		61	GCTACGAGCCCTGAGCGAGCGCGGCG-----GGAGGAGCCCTCAAGCGGAGCAGC	111
Db		69	GCGGCGAGTCCGAGGCGGGCGGCGCGCGGCGGAGGAGGAGACTCTCCAGGAGAACGCGC	128
Qy		112	GCGCCC---GGGCGTCCCGCGGAGACTCTCGGAGGCGGCGAGCGGGGCGCGCAGCGG	168
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Qy		169	CGCGACTGCGCGCGCGCGCAGCTCGCAAATGCGGAGTTGAGCTGACCAGAGTGCCT	228
Db		189	GCGGACTGCGCGCGCGCGCACGTGCGAAATGCGGAGTTGAGCTGACCAGAGTGCCT	248
Qy		229	GAGCAGCGCTCTCTTTCGCGCTCAACCGCGGCGCT---CTTCGACTTCCCGCTCGCGC	285
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Qy		286	GAGCCGCGGAGCAGCGCGGAGTTGGACCGGCTTCAGCCTGTGGCGGTGCGCGCGCC	345
Db		309	GAGCCGCGGAGCAGCGGCTCTGAGGAGCGAGTGCCTTCAGCCCCGCGCGGAGCCGCCACCC	368
Qy		346	CACGGAGCGCGAGCGCGCGGGCGGCCACATTACCGAGTCGTTGGCGCGCGCGACAGC	405
Db		369	CCGGGAGCGCGAGTGCCTGCGGCTCCCACTCTGCCAGCTGGCGCGCGCGGGACAGC	428
Qy		406	GGGCGCTCGAGTCCGCGAGCGCGCGAGCCCGGGGAGAGCGGGCGCCCCCGCGCAGCGCG	465
Db		429	GCGGCCCGAGCCCGCGGGG-----GGGAGCGCG	458
Qy		466	TCTCTCGACGCGCCCGCGCGTCTGAGATGGAGAATAAAGAAACTCTCAAAGGTTG	525
Db		459	CCCTCTGCAGCGCCCGCTTCGCTCGAGAGATGAGAAATAAGAAACCCCTCAAAGAGCTG	518
Qy		526	CACAAGATGGATGCTCCAGAGAAAGAAATGATCAGGGAGAAACTGAGGCAACTCTGT	585
Db		519	CACAAGATGAGATCGCCCGGAGGAGAGATGATCGGGAGAAAGTCAAGGCGACCTGT	578
Qy		586	ATGCCAGCTGGAAGCACGAATGGTTGGAAAAGGAGAAATAGCGAGGGCTGTGTGGTA	645
Db		579	ATSCCGGCTTGAAGCACAGAGTGGTTGGAGAGAGGAGAACAGAGAGGCGCTGTGTGGTG	638
Qy		646	AATCCCAATCCAGTTAAAGGAGATGGATCTGAATGAATCACTTAGCAGCTGAGTCTCCA	705
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Qy		706	GGAGAGGTCCAGCAAGTCCGGCTTCAACAGCTTCCAAAGGCCGAGCGAGTCTCTTCCT	765
Db		699	GGAGAGGGCCAGGACAGTCTCCGTGACACAGCCCCCAAGGGCCGACGAAGCCCATCTCT	758
Qy		766	GGCAACTCCCCATCAGTCTGCAAGTGAATCAGAAATCTCCAGGAGTAAGGAGAAAAAGA	825
Db		759	GGCAGCTCTCGTCAAGGCGCTCGTGAAGCGGHAATCCCCAGGAGTAAGACGGAACGA	818
Qy		826	GTATCCCAAGTGCCTTTTCAGATGCGCAGAAATCACACACCCCGAGAGGCCCTTCAACA	885
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Db 2079 GATGCCAACAGCCGCAACAAGTCAAGTCTGCATATCAACACTGTGTGGAATCTGTGCAAGGC 2138  
Qy 2143 CAAGCAGAGAGTTGGCAGTTGGCAGAGAAATCTAAAGCTGATCCATTTGGTATTTGGT 2202  
Db 2139 CAAGCAGAGAGTTGGCAGTTGGCAGAGAAATCTAAAGCTGATCCATTTGGTATTTGGT 2198  
Qy 2203 GGTGTGATATGCTTAAATTTGATTTCTTGGAAACCAAACTGAATCAAACTATTTGGCAA 2262  
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Qy 2263 GAACCTTTGTCGCCCTTTGCTTTATAGATAGACTGTGTGTTGGAATTTCTGCTGAATTT 2322  
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Qy 2323 TATCCTCATATTTGCTGACTGATGTTTCAAACTGAGCTGTGTTGAAATCAGTATAAG 2382  
Db 2319 TATCCTCATATTTGCTGACTGATGTTTCAAACTGAGCTGTGTTGAAATCAGTATAAG 2378  
Qy 2383 AAGCTGCTGCTCCTTTAACTTTGCTTTGAGTCCATTTGATTAATTTCCACTCAATGGTT 2442  
Db 2379 AAGCTGCTCCTCCTTTAACTTTGCTTTGAGTCCATTTGATTAATTTCCACTCAATGGTT 2438  
Qy 2443 GGCAAACTTTCCAGAGATCTACTGAGTTCTCGAAGATGTTTACTACAGTACCCCAT 2502  
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Qy 2503 GTGTTTTCAAACTTTAGAAATGCTGAGTGTTCAGTTCCTCACTCACTCAACAGGATG 2562  
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Qy 2863 AAGCCAAATGTTTCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 2922  
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Db 3054 TGCTCTGAACACCGAGCTCAGACCGACTCTCCCGAGTCTTCACTCAGTCAAGACCCCA 3113  
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 VERSION AR181002.1 GI:20223035  
 KEYWORDS Location/Qualifiers  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 5539)  
 AUTHORS Johnson,G.L.  
 TITLE Method and product for regulating cell responsiveness to external signals  
 JOURNAL Patent: US 6333170-A 3 25-DEC-2001;  
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ORIGIN

Query Match 64.6%; Score 3387.6; DB 6; Length 5539;  
 Best Local Similarity 83.4%; Pred. No. 0;

Matches 4075; Conservative 0; Mismatches 709; Indels 102; Gaps 16;  
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Qy	1127	TGTTATCGAGAAAAACCTTAAAGAAATTTGAGGTTGAGAGTTGTTCCAGAAAATATCACA	1186	2204	GTGTTGATTAATGTCTTAATTTGTAATCTTTGGAACCAAACTGAATCAAACTATGGGCAAG	2263
Db	1406	TGTTATCGAGAAAAACCTTAAAGAAATTTGAGGTTGAGAGTTGTTCCAGAAAATATCACA	1465	2486	GTGTCGATTAATCTCTTAAGTTGTAATCTTTGGAACCAAACTGAATCAAACTATGGGCAAG	2545
Qy	1187	GTAGGCGTAGCTCAAGGATCAAGCTCCATCTCTGTAAACACATCCAGAAATTTGTTTCAC	1246	2264	AACTCTCTGGCGCTTTGTTCTTATAGATAGACTGTTGGAATTTCTCTGCTGAATTTT	2323
Db	1466	GTAGGCGTAGCTCAAGGATCAAGCTCCATCTCTGTAAACACATCCAGAAATTTGTTTCAC	1525	2546	AACTCTCTGGCGCTTTGTTCTTATAGATAGACTGTTGGAATTTCTCTGCTGAATTTT	2605
Qy	1247	GCATGTCGAATTTCTCATATGTCATCTAGTACTCTTACGCTGAGTTTCAGAAAACA	1306	2324	ATTCCTCATATTTGTCAGTACTGATGTTTCAAGCTGAGCCTGTTGAATTCAGGTTAAGA	2383
Db	1526	GCATGTCGAATTTCTCATATGTCATCTAGTACTCTTACGCTGAGTTTCAGAAAACA	1585	2606	ATTCCTCATATTTGTCAGTACTGATGTTTCAAGCTGAGCCTGTTGAATTCAGGTTAAGA	2665
Qy	1307	GCATAAAGGATGAAGAGAAACAGATGTCTCTATTTGCTTTGTTGGGCATGCTTGATGAG	1366	2384	AGCTGCTCTCCCTCTTTAACTTTGCTTTGTCAGTCCATTAATTTCCCACTCAATGGTTG	2443
Db	1586	GCATAAAGGATGAAGAGAAACAGATGTCTCTATTTGCTTTGTTGGGCATGCTTGATGAG	1645	2666	AGCTGCTCTCCCTCTTTAACTTTGCTTTGTCAGTCCATTAATTTCCCACTCAATGGTTG	2725
Qy	1367	AAAGTCTTACAGTGTGTAAGACGGCTGCAGAACAGCTGCACACCACTGCATGTCAA	1426	2444	GCAAACTTTCCAGAGGATCTACTTTGAGTTCTGCAAGAAATGGTTACTACTAGTACCCCATG	2503
Db	1646	AAAGTCTTACAGTGTGTAAGACGGCTGCAGAACAGCTGCACACCACTGCATGTCAA	1705	2726	GCAAGCTCTCTCGAGGATATATCTGAGCTCTGCCAGGATGGTGACCGAGTGCCTCGCTG	2785
Qy	1427	TTTGGCGAAGAGGTGTAAGAAATAGAGAACCTTTAATATGTCCCTTTGTAGATCTA	1486	2504	TGTTTTCAAACTGTAGAAATGCTGAGTTTCCAGTTTCCACTCACTTCCACAGATGC	2563
Db	1706	TTTGGCGAAGAGGTGTAAGAAATAGAGAACCTTTAATATGTCCCTTTGTAGATCTA	1765	2786	TGTTTTCAAACTGTAGAAATGCTGAGTTTCCAGTTTCCACTCACTTCCACAGATGC	2845
Qy	1487	AGTGAGATCTCATGATTTCTACAGCCAGAGTTGTCAAGTCTCTGGATTCCTCTCTT	1546	2564	GTCCCGCTTTGATGGCTATTTGAGATGAGGTGAGAAATTTGCCGAAGCCATCCAGTTGGGG	2623
Db	1766	AGTGAGATCTCATGATTTCTACAGCCAGAGTTGTCAAGTCTCTGGATTCCTCTCTT	1825	2846	GCGGGGCTCTGATGGCTATTCGCGGATGAGGTAGAAATTTGCCGAGGTCTCCAGCTGGGTG	2905
Qy	1547	CCCTCAGAGCTGCACAGCAGCAAAACCGTACAGCAGCAGCCTTTGGCTGGATCA---CGAA	1603	2624	TAGAACACTTTGGATGTTCAACAGGACAGCTTTTTCAGGACATCTGTTCCCAACAAT	2683
Db	1826	CCCTCAGAGCTGCACAGCAGCAAAACCGTACAGCAGCAGCCTTTGGCTGGATCA---CGAA	1885	2906	TGAGAGACACTGTGGGATGGGCATCAGGACAG---CTTACAGGCGGTGGCCCCCAACAGCT	2962
Qy	1604	GGAACTCAGAGAGCAATTTTAACCTTACTTATTAAGAACTCAGCAAACTCCCTCTGCTT	1663	2684	ATCTGGAACCAACAGAGAACAGTTTCCCTGAGTGCACAGTCCATTTAGAGAAACTTGGAA	2743
Db	1886	GGAACTCAGAGAGCAATTTTAACCTTACTTATTAAGAACTCAGCAAACTCCCTCTGCTT	1945	2963	GTCT-----AGAAACAGCTCCCTTGAGCACACAGTCCATAGAGAGAAACTTGGAA	3013
Qy	1664	ACAAAGATTAGCTCAGAGCATTGATTCAGGTTGTTGGAAATGGAACTCGTTGGCTGCTTAT	1723	2744	AAGGATATGTCCTACAAATTTGAGTGCAGTTTCAGAGACATTTCTGAGAGACTGGCCA	2803
Db	1946	ACAAAGATTAGCTCAGAGCATTGATTCAGGTTGTTGGAAATGGAACTCGTTGGCTGCTTAT	2005	3014	AAGGACTAAGTGTACGAGACTGAGTGCAGCTCGAGGACATTTCTGACAGCTGGCG	3073
Qy	1724	TTTCTAGAACTGGAAATGTAGAGAGATGGCCCTCAGGGTCTTTCCCATGATGTAGTG	1783	2804	GCATTTAGTACAGTCTCTTAGTTTCAACAAACAAACAAACAAACAAACAAACAAACAA	2863
Db	2006	TTTCTAGAACTGGAAATGTAGAGAGATGGCCCTCAGGGTCTTTCCCATGATGTAGTG	2065	3074	GCCTCTCTGATGACTTCCAGCT-----CAACAAACAAACAAACAAACAAACAAACAA	3118
Qy	1784	GGGCGCTGCTGTTGCAATGGGAGAGCACTGGAAATTTCTGGGGGAGCAGTGGAGCA	1843	2864	AGCAATGTTTCAAAACAAAGGAGACCCCAACAGTCAAGTGTGTAAGTCTCTCTCTTAT	2923
Db	2066	GGGCGCTGCTGTTGCAATGGGAGAGCACTGGAAATTTCTGGGGGAGCAGTGGAGCA	2125	3119	AGCCAGCGGTTCAAAACAAAGGAGACCCCAACAGTCAAGTGTGTAAGTCTCTCTCTTGT	3178
Qy	1844	GCCGAGTGGGGAGCCACAGTGGGTCTTCCAGACAGATATCTCAGAGATGTGGTG	1903	2924	CTCATCTTCCCAATTAATGTTTCCAGCTTGTCAACCCCTCTCTTCTTACCCCATCTG	2983
Db	2126	GCTTAAGCGGGAGCGGCGCAGCGGTCTTCCAGCCAGCATCTCAGGGGATGTGGTG	2185	3179	C---TCATGCTCAATTAATGTTTCCAGCACCATCAGCCCTTGTCTCTGCCCCGCTG	3235
Qy	1904	AGGCATGCTCAGCGTTCTGTAATGCTGCTGAGCCCTGCTACAAAGTGTACGTTG	1963	2984	TACAGCTGGCAGTGCACACAGATGTCTTAAGCATAGACTTTCAGGATTCATTCCCTGCA	3043
Db	2186	AGGCATGCTCAGCGTTCTGTAATGCTGCTGAGCCCTGCTACAAAGTGTACGTTG	2245	3236	TCC-----CAGATATTTCTAAGCACAGACCCCAAGGATTTGTTTCCCTGCA	3280
Qy	1964	CTGCTTTAAAAACATTGAGAGCCATGCTGGTATATCTCTTTGCCACAGTTTAGCGAAA	2023	3044	GAATACCTTCTGATCTCTCAACACAGCGCAAGTTTCTCTACAAATTCACAGAAACT	3103
Db	2246	CTGCTTTAAAAACATTGAGAGCCATGCTGGTATATCTCTTTGCCACAGTTTAGCGAAA	2305	3281	AAATACCTTCCGATCTCTCAGACACAGCGCAAGTTCTCTCAATTCAGAGGAACT	3340
Qy	2024	GAATCAACTTCAGAGACTTCCAGCAGTTGTAGACACCACTCTAGTCAATGTGCGAG	2083	3104	GTCTGAAAAACAAAGACTCAGATAAATTTTCCAGCTTTTACTCTAGTCAAGACCTTGC	3163
Db	2306	GAATCAACTTCAGAGACTTCCAGCAGTTGTAGACACCACTCTAGTCAATGTGCGAG	2365	3341	GCTCTGAACACCGAGACTCAGACAGCTCTCCCGAGTCTTCACTCAGTCAAGACCCCCAC	3400
Qy	2084	ATGCCAATAGCCGACAGTCACTGTCCATATCAACACTGTGTGAACTGTGCAAGGCC	2143	3164	CCTCAGTAAATACACAGGCGCAAGCCATCTAGCTACCCAGGTAATACAGTAAAC	3223
Db	2366	ATGCCAATAGCCGACAGTCACTGTCCATATCAACACTGTGTGAACTGTGCAAGGCC	2425	3401	CCTCCAGTAAATACACAGGCGCAAGCCATCTCCGACCCGTTCCGGGCGGTACAGCAAC	3460
				3224	AGGAGATGCCCTCAAAAAATAGCATGACACTTGTGTGAACAGTAGTTCCTCAAAATGTGATG	3283





QY	2930	ATTCCAAATTAATGTTTCCAGCGTTGTCAACCCCTTCTTCTTCTTAACCCAACTGTACCAG	2989
Db	2311	ATGCTCAATTAATGTTTCCAGCACCACTCAGCCCGTGTTCCTCTGCCCCGTGTCTCC---	2367
QY	2990	CTGGCACTCAACAGAGATGCTCTTAAGCATAGACTTTCAGGGATTCTATTCCTCCAGAAATAC	3049
Db	2368	-----CAGATATTTCTTAAGCACAGACCCAGGCATTTGTTTCTTCCGTGAANAATAC	2415
QY	3050	CTTCTGCATCTCTCTAAAACACAGCGCAAGTTTCTCTCAAAATTCACAGAAACTGTCGTG	3109
Db	2416	CTTCCGCATCTCTCTCAGACACAGCGCAAGTTCTCTCTCAAAATTCAGAGAGAACTGCTCTG	2475
QY	3110	AAAACAAAGACTCAGATAAATTTTCCCGAGTCTTTTACTCAGTCAAGCAACCTTGCCCTCCA	3169
Db	2476	AACCCGAGACTCAGAACCCAGCTCTCCCGAGTCTTCACTCAGTCAAGACCCCACTCTCCA	2535
QY	3170	GTAACTATACACAGGCCAAAGCCATCTAGACCTTACCCCAAGTAAATACAAGTAAACAAGGAG	3229
Db	2536	GTAACTATACACAGGCCAAAGCCATCCGACCCGTTCCGGCGAGTACAAGCAAACTAGGGG	2595
QY	3230	ATCCCTCAAAAAATACATGACACTTGTCGAAACAGTAGTTCCTCAAACTGTGATGACAGCT	3289
Db	2596	ACCCCAAAAAATAGTACATGACACTTGATCTGGCGAGTGTCTCCAGGTGTGACGACAGCT	2655
QY	3290	TTGGCTGTAGCACAATAGTAGTAATGCTGTTATACCCAGTGCAGACAGTGTTCACCC	3349
Db	2656	TTGGCGCGCGCGCAACAGTGGCAACCCGTCATACCCAGCGACGACAGTGTTCACGC	2715
QY	3350	CAGTAGGAGAAATCGAGATTAGATGTCAATACAGAGCTCACTCCAGTATTGAGGACC	3409
Db	2716	CGGTGGAGGACAAAGTGCAGGTAGATGTGAACCCGAGCTCAACTCCAGCATCGAGAAC	2775
QY	3410	TTCTTGAAGCATCTATGCCCTTCAAGTGATACAACAGTAACTTTTAAAGTCAGAAGTGTCTG	3469
Db	2776	TTCTTGAAGCATCCATGCCCTTCAAGTGACACGACAGTCACTTTCAAGTCGAAGTGC CGG	2835
QY	3470	TCCTGTCTCTGAAAAGGCTGAAAATGATGATACCTTACAAGATGATGTGAATCATATTC	3529
Db	2836	TCCTCTCTCCGAAAAAGCGGAAATGACACACCTTACAAAGACGAGCTCAATCATATTC	2895
QY	3530	AAAAGTGCAAAAGAGAAAGATGAAAGCTGAAGAAGAAAGCTTTAGCAATTGCATGGCAA	3589
Db	2896	AAAAGTGCAAAAGAAAGATGGAAGCTGAAGAGGAGGAGCTTTAGCGATCGCCATGGCGA	2955
QY	3590	TGTCAGCGTCTCAGGATGCGCTCCCCATAGTTCTCTAGCTGCAGGTGAAAAATGGAGAAG	3649
Db	2956	TGTCAGCGTCTCAGGATGCGCTCCCCATCGTCCCTCAGCTGCAGGTGGAATAATGGAGAAG	3015
QY	3650	ATATCATCATTTTCAACAGGATACACAGAGACTCTACCAGGACATACCAAAAGCAAAAC	3709
Db	3016	ATATTCATCATTTACGACGAGACACACGAGAACTCTTCCAGGACATACCAAAGCGAAAC	3075
QY	3710	AACCGTATAGAGAAGACACTGAATGGCTGAAAGTCAACAGATAGGCGCTGGAGACATTTT	3769
Db	3076	AGCCTTACAGAGAAGACGCTGAGTGGCTGGAAGCCAGCAGATAGGCGCTCGAGACATTTT	3135
QY	3770	CTTCTGTGTATCAGGCTCAAGATGTGGAACTGGAACTTTAATGGCTGTTAAACAGGTGA	3829
Db	3136	CTTCTGTGTATCAGGCTCAAGATGTGGAACTGGAACTTTAATGGCTGTTAAACAGGTGA	3195
QY	3830	CTTATGTCAGAAAACACTCTTCTGAGCAAGAAGTAGTAGTAAGCACTTAAGAGAAGAGA	3889
Db	3196	CTTATGTCAGAAAACACTCTTCTGAGCAAGAAGTAGTAGTAAGCACTTAAGAGAAGAGA	3255
QY	3890	TAAGAACTGATGAGCCACTGTAATCATCCAAACATCATTTAGGATGTGGGAGCCACGTTGTG	3949
Db	3256	TAAGAACTGATGAGCCACTGTAATCATCCAAACATCATTTAGGATGTGGGAGCCACGTTGTG	3315
QY	3950	AGAAAGCAATTAACAATCTCTTCATTTGAATGGATGGCAAGGGGATACGGTGGCTCATTTGC	4009
Db	3316	AGAAAGCAATTAACAATCTCTTCATTTGAATGGATGGCAAGGGGATACGGTGGCTCATTTGC	3375

Qy	4010	TGAGTAAATATGAGAGCCTTCAAGAATACAGTAGTATTAACTACATACAGAACAGTACTCC	4069
Db	3376	TGAGTAAATATGAGAGCCTTCAAGAATACAGTAGTATTAACTACATACAGAACAGTACTCC	3435
Qy	4070	GTGGCCTTTTCGTATCTCCATGAAAAACAAATCAATTCACAGAGATGTCAAAGGTGCCAAATT	4129
Db	3436	GTGGCCTTTTCGTATCTCCATGAGAACCAAGATCAATTCACAGAGATGTCAAAGGTGCCAAATT	3495
Qy	4130	TGCTAATTGACACACACTGTGTACAGACACTAAGAATTCAGATTTTGGAGCTGCAGCCAGGT	4189
Db	3496	TGCTCAATTGACACACCGGTACAGAGCTGAGAAATTCAGACTTTGGAGCTGCAGCCAGGT	3555
Qy	4190	TGGCATCAAAAGGAACTGGTGCAGGAGAGTTTCAGGGACAATTACTGGGGACAATTTGCAT	4249
Db	3556	TGGCATCAAAAGGAACTGGTGCAGGAGAGTTTCAGGGACAATTACTGGGGACAATTTGCAT	3615
Qy	4250	TTATGGCACTGAGGTACTAAGAGGTCAACAGTATGGAAGAGCTGTGATGTATGAGTG	4309
Db	3616	TCATGGCGCCTGAGTCTTAAGAGGTCAACAGTATGGAAGAGCTGTGATGTATGAGTG	3675
Qy	4310	TTGGCTGTGCTATTATAGAATCGCTTGTGCAAAAACACCATCGAATGCAGAAAAACACT	4369
Db	3676	TTGGCTGCGCAATTATAGAATCGCTTGTGCAAAAACACCTTGGAAATGCAGAAAAACACT	3735
Qy	4370	CCAATCATCTTGCTTTGATATTTAAGATTCCTTAGTGCAACTACTGTCTCCATCGATCCCTT	4429
Db	3736	CCAATCATCTCGCCTTGATATTTAAGATTCCTTAGCGCAACTACTGCAACCGTCCATCCCGT	3795
Qy	4430	CACATTTGCTCTCGTGGTTACGAGATGTGCTCTTTCGTGCTTTTAGAACTTCAACCTCAGG	4489
Db	3796	CACACCTGTCCCTGGTTTACGAGATGTGCTCTTTCGTGCTTTTAGAACTTCAACCTCAGG	3855
Qy	4490	ACAGACCTCCATCAAGAGAGCTACTGAAGCATCCAGTCTTTTCGTACTACATGTTAG	4545
Db	3856	ACCGGCTCTCGTCAAGAGAGCTGTGAAACATCCGGTCTTCCTGATCCACCTGGTAG	3912

RESULT 11

AX803383	AX803383	2103 bp	DNA	linear	PAT 24-NOV-2003
LOCUS	AX803383				
DEFINITION	Sequence 45 from Patent WO03000901.				
ACCESSION	AX803383				
VERSION	AX803383.1	GI:38502046			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				

## REFERENCE

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NLFIEWAGGSVAHLSKYGAFKESVINYTEQLRGLSYLHENQIITHRDVKGANLIL  
DSTGQRLRIADFGAARLASKTGAGFEGOLGTTAFMAPEVLRGQYGRSCDVWSV  
CAIITEMACKPPNNAEKHSHLALIFKIASATAPSPSHSPGLRDVAURCLELQF  
QDRPESALLKHPVETTW"

## ORIGIN

Query Match 39.8%: Score 2086.8: DB 6: Length 2103:

Query Match	2.0%	2000
Best Local Similarity	99.8%	Pred. No. 0:

Best Local Similarity 99.8%, Freq: NO: 0;  
Matches 2101: Conservative 2: Indels 3: Gaps 1;  
Matches 2101: Mismatches 0: Indels 3: Gaps 1;

2437 ATGGTTGGCAACCTTCCAGAGGATCTACTTGAGTTCTGCAAGAAATGGTTACTACAGTA 2496

QY Z437 AIGG1GGCAAC11CCAGAAAGGAC1AC11GAS11C1CAGAAAGG1AC1ACAG1A Z4390

1 ATGTTGGCAAACCTTCCAGAGGATCTACTTGAGTTCTGCCAGAAATGGTACTACAGTA 60

DD T HIGGINS

2497 CCCCATGTGTTTCAAACCTGTTAGAAATGCTGAGTGTTCCAGTTCACCTCACC 2556

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Db 61 CCCCATGTGTTTCAAACTGTTAGAAATGCTGAGTGTTTCCAGTTCCACTCACATTCACC 120

2000

2557 AGGATGCGTCGCCCGTTTGATGGCTATTGCAGATGAGGTGAAATTGCCGAGCCATCCAG 2616

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Db 121 AGGATGCGTCTGATGGCTATTGCAGATGAGGTGGAAATTGCCGAGCCATCCAG 180

QY 2617 TTGGCGTAGAGACACTTTGGATGGTCAACAGGACAGCTTCTGCAGGCATCTGTTCCC 2676

1. *Chlorophyll a* (Chl a) content was determined using a spectrophotometer (Shimadzu UV-1601) at 663 nm. The concentration of Chl a was calculated using the following formula:  $\text{Chl a (mg/L)} = \frac{\text{Absorbance at 663 nm} \times 1000}{\text{Path length (cm)}} \times \frac{1}{0.0206}$ .

Db 181 TTGGCGTAGAGACACTTTGGATGGTCAACAGGACAGCTTCTTGCAGGCATCTGTTCCC 240

QY 2677 AACAACTATCTGGAAACCAACAGAGAACAGTTCCTGAGTGCACAGTCCATTAGAGAAA 2736

[illegible]

Db 241 AACAACTATCTGGAAACACAGAGAACAGTTCCTGAGTGACAAATCCATTAGAGAA 300

[illegible]

2737 ACTGGAAAAGGATTATGTGCTACAAAATTGAGTGCCAGTTCTGAGAGA 2796

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## RESULT 12

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 DEFINITION Mus musculus MEK kinase mRNA, complete cds.  
 ACCESSION L31103  
 VERSION L31103.1 GI:293729  
 KEYWORDS MEK kinase.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 3244)  
 LANGE-CATTER, C.A., Pleiman, C.M., Gardner, A.M., Blumer, K.J. and  
 Johnson, G.L.  
 TITLE A divergence in the MAP kinase regulatory network defined by MEK  
 kinase and Raf  
 JOURNAL Science 260 (5106), 315-319 (1993)  
 MEDLINE 93227040  
 PUBMED 8385802  
 COMMENT Original source text: Mus musculus (strain BALB/c, sub\_species domesticus) (Library: Stratagene) post natal day 20 brain cDNA to mRNA.

## FEATURES

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## ORIGIN

Query Match 37.58; Score 1969.2; DB 10; Length 3244;  
 Best Local Similarity 82.78; Pred. No. 0;  
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LOCUS Sequence 1 from patent US 5753446.  
DEFINITION AR008276  
ACCESSION AR008276  
VERSION AR008276.1 GI:3967385  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3260)  
AUTHORS Johnson,G.I.  
TITLE Mitogen ERK kinase (MEKK) assay  
JOURNAL Patent: US 5753446-A 1 19-MAY-1998;  
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DEFINITION Sequence 1 from patent US 5854043.
ACCESSION AR068730
VERSION   AR068730.1  GI:6000937
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 3260)
AUTHORS  Johnson,G.L.
TITLE    MEKK-related signal transduction kinases
JOURNAL  Patent: US 5854043-A 1 29-DEC-1998;
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ORIGIN

Query Match      37.3%; Score 1955.6; DB 6; Length 3260;
Best Local Similarity 82.7%; Pred. No. 0;
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ACCESSION AR085072  
VERSION AR085072.1 GI:10011843  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3260)  
AUTHORS Johnson,G.L.  
TITLES Methods for regulating MEK protein activity  
JOURNAL Patent: US 5981265-A 1 09-NOV-1999;  
FEATURES Location/Qualifiers  
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Query Match 37.3%; Score 1955.6; DB 6; Length 3260;  
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; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
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; TITLE OF INVENTION: HUMAN MEK PROTEIN AND NUCLEIC ACID MOLECULES
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; FILE REFERENCE: CPI-085CPPC
; CURRENT APPLICATION NUMBER: US/09/423,890
; CURRENT FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: USSN 60/078,153
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: USSN 60/099,165
; PRIOR FILING DATE: 1998-09-04
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; NAME/KEY: CDS
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US-09-423-890-7

Query Match 65.1%; Score 3417; DB 4; Length 5253;
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RESULT 5  
US-08-049-254-1

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Sequence 1, Application US/08049254  
Patent No. 5405941  
GENERAL INFORMATION:  
APPLICANT: Johnson Ph.D., Gary L.  
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL  
TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SHERIDAN ROSS & MCINTOSH, P.C.  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: CO  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: IBM PC compatible  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/049,254  
FILING DATE: 19930415  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kovarik Esq., Joseph E.  
REGISTRATION NUMBER: 33,005  
REFERENCE/DOCKET NUMBER: 2879-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
TELEX: 467377

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3260 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MEKK  
STRAIN: murine  
IMMEDIATE SOURCE:  
LIBRARY: mouse liver  
CLONE: MEKK cDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..485  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 486..2501  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 2502..3260  
US-08-049-254-1

Query Match 37.3%; Score 1955.6; DB 1; Length 3260;  
Best local Similarity 82.7%; Pred. No. 0;  
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

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Db 1875 CCAACATCATTCGGATGTGGGGCCAGTGTGAGAGAGCAATTAACATCTTCTTCAIT 1934  
QY 3976 GAATGATGCGAGGGGATGGTGTCTTATTTGCTGAGTAATATGAGCGCTTCAAGAA 4035  
Db 1935 GAGTGGATGGCGGAGGATCTGTGGCTCACCTCTTGAATAATAGGAGCTTTCAAGGAG 1994  
QY 4036 TCAGTAGTTATTAACTACAGTGAACAGTGTACTCCGTCGCTTCTGATCTCCATGAAC 4095  
Db 1995 TCAGTGTCTAATTAACACTAGAGAGTACTCGGTGGCTTCTTCTTCTCCAGAGAAC 2054  
QY 4096 CAAATCATTCACAGAGATGCAAGGTGCAATTTCTTAATGACAGCACTGGTCAGAGA 4155  
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QY 4156 CTGAAGATTCAGATTTGAGCTGAGCGGAGTGGATCAAAAGGAGTGGTCAGGA 4215  
Db 2115 CTGAAGATTCAGACTTTGAGCTGCTCCAGGTGGATCAAAAGGAGTGGTCAGGA 2174  
QY 4216 GAGTTTCAGGAGCAATTTACTGGGCAATTTGATGGCACTGAGGTACTAAGAGGT 4275  
Db 2175 GAGTTTCAGGAGCAATTTACTGGGCAATTTGATGGCACTGAGGTACTAAGAGGT 2234  
QY 4276 CAACAGTATGAGAGGAGCTGTGATGAGTGTGGCTGTGCTATTATGAATGGCT 4335  
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QY 4336 TGTGCAAAACACCATGGAATGAGAGAGAGAGAGTCAATCTCTGCTTTGATATTAG 4395

Db 2295 TGTGCAAAACACCTTGGATGAGAGAGAGAGAGAGTCAATCTATCTCGCTTGTATTAG 2354  
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Db 2355 ATTCGTAGTGAACACTACTGCTTCAATGATGATCCCTTCAATTTGCTCTCTGTTTACAGAT 2414  
QY 4456 GTGCTCTTCTGTTTGTAGAACTTCACTCAGGAGAGAGTCCATCAAGAGAGCTTACTG 4515  
Db 2415 GTGCTCTTCTGTTTGTAGAACTTCACTCAGGAGAGAGTCCATCAAGAGAGCTTACTG 2474  
QY 4516 AAGCATCCAGTCTTCTGATCTACTGATGATGATGATGATGATGATGATGATGATGATGATG 4575  
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Db 2535 AGGATGCTCAACAG 2594  
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QY 4692 ATTGACAAATCATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 4750  
Db 2654 ATTGACAAATCATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 2713  
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Db 2714 ACTGTAACATGCTCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2773  
QY 4811 CAGTACTTAATTCAG 4864  
Db 2774 CAGTACTTAATTCAG 2825

## RESULT 6

US-08-472-934-1  
; Sequence 1, Application US/08472934  
; Patent No. 5753446  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, GARY L.  
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL  
; TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lahive and Cockfield  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,934  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/440,421  
; FILING DATE: 15-May-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/354,516  
; FILING DATE: 21-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 5,405,941  
; FILING DATE: 15-Apr-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/323,460  
; FILING DATE: 14-Oct-1994  
; PRIOR APPLICATION DATA:

```
APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIORITY INFORMATION:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr. Esq.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: CPI-004DVCP2
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3260 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MEKK
STRAIN: murine
IMMEDIATE SOURCE:
LIBRARY: mouse liver
CLONE: MEKK cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..485
NAME/KEY: CDS
LOCATION: 486..2501
NAME/KEY: 3'UTR
LOCATION: 2502..3260
US-08-472-934-1

Query Match
Best Local Similarity 37.3%; Score 1955.6; DB 1; Length 3260;
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

QY 1996 TATACCTCTTGGCCACAGTTTAGCGGAAAGAAATCAAACTTCAGAGACTTCTCCAGGCGAGTT 2055
Db 1 TACACTCTTGGCCACAGTTTGGCGAAGAAATCAAACTTCAGAGACTTCTCCAGGCGAGTT 60

QY 2056 GTAGACACCATCTCTAGTCAAAATGTGCAGATGCCATAGCGGCACAAAGTCAGTGTCCATA 2115
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QY 2116 TCAACACTGTGGAACTGTGCAAGGCCCAAGCAGAGAGTTGGCAGTTGGCAGAGAAATA 2175
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QY 2176 CTAAAGCTGGATGCCATTTGGTATTTGGTGTGTGATTATGTCTTAAATTTGTTATCTTGA 2235
Db 180 CTAAAGCTGGGTCCTATCGGGTGGTGTGTGATTATGTCTTAAATTTGTTATCTTGA 239

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Db 240 AACCAAGCTGAATCAACAAATGGCAAGAACTTCTGGCGGCTTGTCTTATAGACAGG 299

QY 2296 CTGTTCTTGGAAATTCCTCTGAATTTTATCTCATATTTGTCAGTACTGATGTTTCAAA 2355
Db 300 TTGCTGTGGAAATTCCTCTGAATTTTATCTCATATTTGTCAGTACTGATGTTTCAAA 359

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Db 360 GCTGAGCCTGTGAATCAGGATAGAGAGCTGTCTCTCTTAACTTGTCTTGGAG 419

QY 2416 TCCATTGATAATTCACACTCAATGGTGGCAAACTTTCCAGAGAGATCTACTTTGAGTTCT 2475
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QY 2476 GCAAGATGGTTACTACAGTACCCCATGTTTTCAAAACCTGTTAGAAATGCTGAGTGT 2535

; APPLICATION NUMBER: PCT/US94/11690
; FILING DATE: 14-OCT-1994
; PRIORITY INFORMATION:
; APPLICATION NUMBER: PCT/US94/04178
; FILING DATE: 15-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Giulio A. DeConti, Jr. Esq.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: CPI-004DVCP2
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MEKK
; STRAIN: murine
; IMMEDIATE SOURCE:
; LIBRARY: mouse liver
; CLONE: MEKK cDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..485
; NAME/KEY: CDS
; LOCATION: 486..2501
; NAME/KEY: 3'UTR
; LOCATION: 2502..3260
; US-08-472-934-1

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600 GAAATTCGAGGTCATCCAGTGGGTGTGAGGACACTGTGGATGGCATCAGGACAG- 658
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2776 TCAGAGGACATTTCTGAGAGACTGGCCAGCATTTTCAGTAGACCTTCTAGTTCACAAACA 2835
768 TCGAGGAGACATTTCTGACAGACTGGCGGGCTCTCTGTAGACTTCCCACT----- 819
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820 -----CAACAACAACAGAGCAACCAAGGCCAGCGGTTCAACAAAGGACAGACCCAC 872
2896 AGTCAGTGTGTAACCTCTCTCTTATCTCATCATNTCCAAATTAATGTTTCAGGCTTG 2955
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930 TCAGCCCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 974
3016 CATGACTTCAGGATTCATTCCTGCGAATTAACCTTCTGCTATCTCTCTCTCTCTCTCTCT 3075
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3196 AGACTTACCCAGTAACTACAAGTAAACAGGAGATCCCTCAAAATAATAGCATGACACTT 3255
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Db 1575 ATCGTCCCTCAGCTCGAGGTTGAAATGGAGAGATATTTCAATCATTTACAGAGACACA 1634  
Qy 3676 CCAGAGACTCTTACAGGACATACCAAGCAAAACACCGTATAGAGAGACACTGAATGG 3735  
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Qy 3856 CAAGAAGAGTATAGAGACATTAAGAGAGAGATAAGATGATGAGCCATCTGATCAT 3915  
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Qy 3916 CCAACATCATTTAGATGTTGGAGCCAGCTGTGAGAGAGCAATTAACAATCTTCTCAT 3975  
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Qy 4096 CAAATCATTTACAGAGATGTCAAAGTGCCAAATTTGCTTAATGACAGCACTGGTCAGAGA 4155  
Db 2055 CAGATCATTTACAGAGACGTCAAAGTGCCAAATTTGCTTAATGACAGCACTGGTCAGAGA 2114  
Qy 4156 CTAAGAAATTCAGATTTGGAGCTGACGAGGTTGGCATCAAAAGGAACTGGTCAGAGA 4215  
Db 2115 CTGAGAAATTCAGATTTGGAGCTGTCGCGAGTTGGCATCAAAAGGAACTGGTCAGAGA 2174  
Qy 4216 GAGTTTCAGGAGCAATTAATGCGGCAATTTGATGTCACCTGAGGTACTAAGAGT 4275  
Db 2175 GAGTTTCAGGAGCAATTAATGCGGCAATTTGATGTCACCTGAGGTACTAAGAGT 2234  
Qy 4276 CAAAGATGGAAGAGGCTGTGATGATGAGTGTGGCTGTGCTATTATAGAAATGCT 4335  
Db 2235 CAGCAGTATGTAAGAGCTGTGATGATGAGTGTGGCTGTGCTATTATAGAAATGCT 2294  
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Db 2295 TGTGCAAAACCCATGGAATGAGAAACACCTCCAATCATCTTGTGATATTTAAG 2354  
Qy 4396 ATTGCTAGTCAACTACTGTCTCATCGATCCCTTCATTTGCTCTCTGTTTACAGAT 4455  
Db 2355 ATTGCTAGTCAACTACTGTCTCATCGATCCCTTCATTTGCTCTCTGTTTACAGAT 2414  
Qy 4456 GTGCTCTTCTGTTTGTAGAACTTCAACCTCAGAGAGAGCTTCAATCAAGAGAGTACTG 4515  
Db 2415 GTGCTCTTCTGTTTGTAGAACTTCAACCTCAGAGAGAGCTTCAATCAAGAGAGTACTG 2474  
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Db 2475 AAGCATCCAGTCTTCTGTTTGTATCATGATGAGCAATTTATGAGATCAACTACAGTAGAAG 2534  
Qy 4576 AGGATGCTCAACAG 4631  
Db 2535 AGGATGCTCAACAG 2594  
Qy 4632 CCATGATGCCACTGAACAGCTATGAACAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAG 4691  
Db 2595 CCCTCAGCCACTGAACAGGAG 2653

Qy 4692 ATTGCAAAATCATGATCTCTTACCTAAGCTCAGTATGCA-AAAGCCAAACTAGTGCAGAA 4750  
Db 2654 ATTGCAAAATCATGATCTCTTACCTAAGCTCAGTATGCAACATCTACAGCTCTGCAGGA 2713  
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Db 2774 CATGACTAAAGAACAGAGACATAATTTA--TTTTTGGAGCACTTTTTCAGCTA 2825

## RESULT 7

US-08-323-460A-1  
; Sequence 1, Application US/08323460A  
; Patent No. 5854043  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, GARY L.  
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL  
; TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH  
; STREET: 1700 LINCOLN STREET, SUITE 3500  
; CITY: DENVER  
; STATE: CO  
; COUNTRY: USA  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/323,460A  
; FILING DATE: 14-OCT-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/049,254  
; FILING DATE: 14-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOVARIK, JOSEPH E.  
; REGISTRATION NUMBER: 33,005  
; REFERENCE/DOCKET NUMBER: 2879-1-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 303/863-9700  
; TELEFAX: 303/863-0223  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3260 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEetical: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: MEKK  
; STRAIN: murine  
; IMMEDIATE SOURCE:  
; LIBRARY: mouse liver  
; CLONE: MEKK cDNA  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: 1..485  
; NAME/KEY: CDS  
; LOCATION: 486..2501  
; NAME/KEY: 3'UTR  
; LOCATION: 2502..3260  
; US-08-323-460A-1

Query Match 37.3%; Score 1955.6; DB 2; Length 3260; Best Local Similarity 82.7%; Pred. No. 0; Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;			
QY	1996	TATACCTCTTGCACAGTTTAGGGGAAAGAAATCAAACTTCAGAGACTTCTCCAGCCAGTT	2055
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QY	2056	GTAGACACCATCTCTAGTCAAAATGTGCAGATGCCAATAGCCGACAAAGTCAGTGTCCCAT	2115
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QY	2116	TCMAACTGTGTGAATGTGCAAGCCCAAGCAGAGAGATTGGCAGTTGGCAGAGAAATA	2175
DB	120	TCTACAGTGTGGAATCTGCAAGGCCCAAGCAGAGAGCTGGCGTTGGGAGAGAAATA	179
QY	2176	CTAAAAGCTGGATCCATTTGATTTGGTGTGTTGATTATGTCTTAAATGTATTCTTGA	2235
DB	180	CTTAAAGCTGGTCCATCGGGTTGGTGTGCGATTACGTTTAAAGTTGTAATCTTGA	239
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DB	240	AACCAAGCTGAATCAAACTAATTTGGCAAGAACTTTTGGCCGCTTTTGTCTTATAGACAG	299
QY	2296	CTGTTGTGGAATTTCTCTGCTGAATTTTATCTCTCATATTGTGAGTACTGATGTTCAAA	2355
DB	300	TTCTCTGTGGAATTTCTCTGCTGAATTTTATCTCTCATATTGTGAGTACTGATGTTCAAA	359
QY	2356	GCTGAGCTGTGGAATTCAGGTATAAGAGCTGCTCTCCCTCTTAACTTTGCTTTGAC	2415
DB	360	GCTGAGCTGTGGAATTCAGGTATAAGAGCTGCTCTCCCTCTTAACTTTGCTTTGCAA	419
QY	2416	TCCATTGATTAATTCACACTCAATGTTGGCAAACTTTCCAGAGGATCTACTGTAGTTCT	2475
DB	420	TCCATTGATTAATTCACACTCGATGTTGGCAAACTTTCCAGAGGATATCTGAGCTCT	479
QY	2476	GCAAGAAATGTTTACTACAGTACCCCATGTTGTTTCAAACTGTGAAATGCTGAGTGT	2535
DB	480	GCCAGGATGTGACCGCAGTGCCCGCTGTGTTTCCAACTGTGTAACCATGTTAATGCT	539
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QY	2596	GAAATTCGCAAGCCATCCAGTTGGCGTGAAGACACTTTGATGTTCAACAGACAGC	2655
DB	600	GAAATTCGCGAGTCTACAGCTGGGTGTGGAGCACTGTGATGGGATCAGGACAG-658	
QY	2656	TTCTTGAGGCATCTGTTCCCAACAATATCTGGAACCCACAGAACAGTTCCTCCCTGAG	2715
DB	659	--CTTACAGCCGTTGGCCCGCCACAGCTGTCT-----AGAAACACAGCTCCCTTGAG	707
QY	2716	TGCACAGTCCATTTAGAGAAACTGGAAAGGATTATGCTACAAATTTAGTGCAGT	2775
DB	708	CACACAGTCCATAGAGAGAAACTGGAAAGGATTAAGTCTACAGACTGAGTGCAGC	767
QY	2776	TCAGAGACATTTCTGAGAGACTGGCCAGCATTTAGTAGGACCTTCTAGTTCAACAACA	2835
DB	768	TCGAGGACATTTCTGACAGCTGGCCGGCTCTGTAGGACTTCCAGCT-----819	
QY	2836	ACAACACACACACACAGAGCACCAAGCCATGTTTCAACAAAGGACAGCCCCAC	2895
DB	820	-----CACACACACACACACCAAGCCAGCGGTTCAACAAAGGACAGCCCCAC	872
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DB	873	AGTCAGTGTGTAATCTCTCTCTTTGTC--TCATGCTCAATTAATGTTTCCAGCACC	929
QY	2956	TCACCCCTCTCTCTTCAACCCATCTGTACCAGCTGGCACTGCAACAGATGTTCTTAAG	3015
DB	930	TCAGCCCTCTCTCTCTGCCCCCTCTGTC-----CAGATATTTCTAAG	974
QY	3016	CATAGACTTCAGGATTCATTTCCCTGCGAATAACCTTCTGCACTCTCCTCAACACAGCGC	3075
DB	975	CACAGACCCAGCGATTTGTTCCTGCAAAATACCTTTCGCACTCTCCTCAGACACAGCGC	1034
QY	3076	AAGTTTTCTCTCAATTTCCACAGAAATGTCCTGAAACAAAGACTCAGATAAATTTCC	3135
DB	1035	AAGTTCTCTCAATTTCCAGAGAACTGCTCTGAAACCGAGACTCAGACAGCTCTCC	1094
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DB	1095	CCAGTCTTCACTCAGTCAAGACCCCACTCCAGTAAACATACACAGGCGCAAGCCATCC	1154
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DB	1155	CGACCCCTTCCGGCAGTACAGCAAACTAGGGAGCCCAAAAGTATGATGACACTT	1214
QY	3256	GATCTGAACAGTATGTTCCAAATGTGATGACAGCTTTGGCTGTAGCAACATATGATTAAT	3315
DB	1215	GATCTGGCAGTGTCTCCAGTGTGACAGCTTTGGCGCGCGCAACAGTGGCAAC	1274
QY	3316	GCTGTTATACCCAGTACAGAGACAGTTCACCCAGTAGAGAGAAATGCAGATAGAT	3375
DB	1275	GCCCTCATACCCAGCGAGACAGTGTTCACGCCGTGGAGGACAAAGTGCAGTTAGAT	1334
QY	3376	GTCAATACAGAGCTCAACTCCAGTATTGAGGACCTTTTGAAGCATCTATGCTTCAAGT	3435
DB	1335	GTGAACCCAGCTCAACTCCAGCATCGAGGACCTTCTTGAAGCATCCATGCTTCAAGT	1394
QY	3436	GATCAACAGTAACTTTTAAAGTCAAGTGTCTGCTCTCTCTGAAAAGGCTGAAAT	3495
DB	1395	GACACGACAGTCACTTTCAAGTCCGAAGTCCCGCTCTCTCTCGGAAAAGGCGCAAAAT	1454
QY	3496	GATGATACCTCAAAAGATGATGTAATCAATAATCAAAAGTGCAAAAGAGATGGAAGCT	3555
DB	1455	GACGACCTCAAAAGACGCTCAATCATATCAAAAGTGCAAAAGAGATGGAAGCT	1514
QY	3556	GAAAGAGAGAAAGCTTTAGCAATGTCATGCGCAATGTGAGCTCTCAGGATGCCCTCCC	3615
DB	1515	GAAAGAGAGAGGCTTTAGCGATCGCATGCGGATGTGAGCTCTCAGGATGCCCTCCC	1574
QY	3616	ATAGTCTCTCAGCTGAGGTTGAAATGGAGAAATATCATATTTTCAACAGGATACA	3675
DB	1575	ATGTTCTCTCAGCTGAGGTTGAAATGGAGAAATATCATATTTTCAACAGGATACA	1634
QY	3676	CCAGAGCTCTACAGGACATACCAAGCAAAACCAACCGTATAGAGAGACATGATGG	3735
DB	1635	CCAGAACTCTTCCAGGACATACCAAGCGAAACAGCTTTACAGAGAGACGCTGAGTGG	1694
QY	3736	CTGAAAGCTCAACAGATAGGCTTTGGAGCATTTTCTTCTGTTATCAGGCTCAAGATGTG	3795
DB	1695	CTGAAAGCCAGAGATAGGCTTCGGAGCATTTTCTTCTGTTTACAGGACAGATGTG	1754
QY	3796	GGAACTGGAACTTTAATGGCTGTAAACAGGTGACTTATGTGAGAAACACATCTTCTGAG	3855
DB	1755	GGAACTGGAACTTTAATGGCTGTAAACAGGTGACTTATGTGAGAAACACATCTTCTGAG	1814
QY	3856	CAAGAGAGTATAGTAGAGCACTAAGAGAGAGATAGAAATGATGAGCCATCTCAATCAT	3915
DB	1815	CAGGAGGAGGTTGGAGAGCCCTGAGGAGAGATCCGGATGATGGGTGCTCAACCAT	1874
QY	3916	CCAAACATCATTTAGGATTTGGGAGCCACGTTGTGAGAGAGCAATTAACAATCTTCTTCAAT	3975
DB	1875	CCAAACATCATTTAGGATTTGGGAGCCACGTTGTGAGAGAGCAATTAACAATCTTCTTCAAT	1934
QY	3976	GAATGATGGCAGGGGATCGTGGCTCAATTTGCTGATTAATATGAGCCCTTCAAGAA	4035
DB	1935	GAGTGGATGGCGGAGGATCTGTGGCTCACTCTTTGAGTAAATACGGAGCTTTCAAGAG	1994
QY	4036	TCAGTAGTATTAACTACACTGAACAGTTACTCCGTGGCCCTTTGCTATCTCCATGAAAC	4095
DB	1995	TCAGTCTGCTAATTAACACTGAGCAGTTACTGCGTGGCCCTTTCTCTATCTCCACGAGAC	2054
QY	4096	CAAAATCATTCAGAGATGTCAAAGGTGCCAATTTGCTTAATGTACAGCACTGGTCAGAGA	4155



2055 CAGATCATTCAGAGACGCTCAAAGGTGCCAACCTGCTCATTTGACAGCACGGTCAGAGG 2114  
QY 4156 CTAAGAAATGAGATTTTGGAGCTGACCGAGGTGGCATCAAAGGAACCTGGTGACGGA 4215  
Db 2115 CTGAGAAATGAGATTTTGGAGCTGCTCCAGGTGGCATCAAAGGAACCGGTGACGGA 2174  
QY 4216 GAGTTTCAGGACAAATTAAGTGGGCAATTCGATTTATGACCTGAGGTAAAGAGT 4275  
Db 2175 GAGTTCCAGGACAGTACTGCGGCAATTCGATTTATGACCTGAGGTAAAGAGT 2234  
QY 4276 CAACAGTATGAAGAGCTGTGATGTATGGAGTGTGGCTGTGCTATTTATAGAAATGGCT 4335  
Db 2235 CAGCAGTATGGAGAGCTGTGATGTATGGAGTGTGGCTGTGCTATTTATAGAAATGGCT 2294  
QY 4336 TGTGCAAAACCAACCATGGAATGAGAAACCACTCAATATCTTGTGCTTGTATTAAG 4395  
Db 2295 TGTGCAAAACCACTTGAATGAGAAACCACTCAATATCTTGTGCTTGTATTAAG 2354  
QY 4396 ATTGCTAGTGAACCTGCTCCATCGATCCCTTCACATTTGTCTCTGCTGTTTACGAGAT 4455  
Db 2355 ATTGCTAGTGAACCTGCTCCATCGATCCCTTCACATTTGTCTCTGCTGTTTACGAGAT 2414  
QY 4456 GTGGCTCTCTGTTGTTTGAACCTCAACCTCAGGACGACCTCCATCAAGAGAGTACTG 4515  
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QY 4516 RAGCATCAGTCTTCTGCTACTGATGAGCAATTTGACATCACTCACTCACTAGTAGAAC 4575  
Db 2475 AAACATCCCGCTCTTCCGTACCACTGTTGTTTGAATTTGTTTCACTGCTCTTAAGGAGAC 2534  
QY 4576 AGGATGCTCAACAAG 4631  
Db 2535 AGGATATCAACCGGAG 2594  
QY 4632 CATGATGCTGCTGACACCTATGACGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4691  
Db 2595 CCGTACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2653  
QY 4692 ATTGACAAATCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4750  
Db 2654 ATTGACAAATCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2713  
QY 4751 ACTGTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4810  
Db 2714 ACTGCAACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2773  
QY 4811 CATGACTAAATTCAG 4864  
Db 2774 CATGACTAAATTCAG 2825

## RESULT 8

US-08-461-146C-1  
; Sequence 1, Application US/08461146C  
; Patent No. 5981265  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, GARY L.  
; TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lahive and Cockfield  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/461,146C  
; APPLICATION NUMBER: US/08/461,146C

; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/354,516  
; FILING DATE: 21-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/049,254  
; FILING DATE: 15-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/323,460  
; FILING DATE: 14-OCT-1994  
; APPLICATION DATA: PCT/US94/11690  
; APPLICATION NUMBER: PCT/US94/11690  
; FILING DATE: 14-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/04178  
; FILING DATE: 15-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KASA, Catherine J.  
; REGISTRATION NUMBER: P41,106  
; REFERENCE/DOCKET NUMBER: CPI-004CN3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3260 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: MEKK  
; STRAIN: murine  
; IMMEDIATE SOURCE:  
; LIBRARY: mouse liver  
; CLONE: MEKK cDNA  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: 1..485  
; NAME/KEY: CDS  
; LOCATION: 486..2501  
; NAME/KEY: 3'UTR  
; LOCATION: 2502..3260  
; US-08-461-146C-1

Query Match 37.3%; Score 1955.6; DB 2; Length 3260;  
Best Local Similarity 82.7%; Pred. No. 0;  
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

QY 1996 TATACCTCTTGGCCACAGTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2055  
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Db 61 GTACACACTATCTTGTCAAGTGTGACAGAT-CCACAGCGCGCACAGTCAAGTGTCCATA 119  
QY 2116 TCAACACTGTGGAACTGTGCGCAAGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2175  
Db 120 TCTACAGTGTGGAACTCTGCAAGGGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179  
QY 2176 CTAAAGCTGATCCATTGGTATTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2235  
Db 180 CTTAAAGCTGGTCCATCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 239  
QY 2236 AACCAAACTGAATCAAACTGAATGGCAAGAACTCTTCTTGGCGCGCTTCTTCTTATAGATAGA 2295  
Db 240 AACCAAGCTGAATCAAACTGAATGGCAAGAACTCTTCTTGGCGCGCTTCTTCTTATAGACAGG 239  
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Db 300 TTGCTGTTGGAAATTTCTTGCTGAATCTATCTCATATGTCAGTACTGATGTCACAA 359  
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Db 360 GCTGAGCCTGTTGAAATCAGGTATAGAAAGTGTGTCCTCTTAACTTTGCTTTGCGAG 419  
QY 2416 TCATTGTGATAATTCCTCACTCAATGCTTGGCAACTTTTCCAGAGGATCTACTTCAGTTCT 2475  
Db 420 TCATTGTGATAATTCCTCACTCAATGCTTGGCAACTTTTCCAGAGGATCTACTTCAGTTCT 479  
QY 2476 GCAAGAAATGGTTACTACAGTACCCCATGTTGTTTCAAAATCTGTTAGAAATGCTCAGTTT 2535  
Db 480 GCCAGGATGGTGACCGCAGTGCCTGTTTCCAAAGCTGTTAAACCATGCTTAAATGCT 539  
QY 2536 TCCAGTTCCACTCACTTCCACAGGATGCTGCGCTTTGATGGCTATTCAGATGAGTG 2595  
Db 540 TCTGCTCTCACCCATTCACAGGATGCGCGGCTCTGATGGCTATTCGCGGATGAGGTA 599  
QY 2596 GAAATTCGCGAAGCCATCCAGTTGGCGGTAGAAGACATTTGGATGGTCAACAGGACAGC 2655  
Db 600 GAAATTCGCGAGGTCACTCCAGTGGGTGTGGAGGACATGTTGGATGGSCATCAGACAG- 658  
QY 2656 TTCCTGAGGCTATCTGTTCCCAACAACTATCTGGAACCAACAGAGAACAGTTCCCTTGAG 2715  
Db 659 --CTTACAGGCGGTGGCGCCCAACCACTGCT-----AGAAACAGCTCCCTTGAG 707  
QY 2716 TGCAAGTCCATTTAGAGAAATCTGAAAGAGATTTATGCTCAAAATTCAGTGCCAGT 2775  
Db 708 CACACAGTCCATAGAGAGAAATCTGAAAGAGACTAAGTGTACGAGACTGATGCCAGC 767  
QY 2776 TCAGAGGACATTTCTGAGAGACTGCCAGCATTTTCAGTAGGACCTTTAGTTTCAACAA 2835  
Db 768 TCGGAGGACATTTCTGACAGACTGGCGCGCTCTCTGTAGACTTCCAGCT----- 819  
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Db 820 -----CAACAAACACAGACAAACAAAGCCAGCGTTCAACAAAGGAGCAGCCCAAC 872  
QY 2896 AGTCAGTGTGAACTCCTCTCTTTATCTCATCTGATCCCAATTAATGTTTCCAGCCTTG 2955  
Db 873 AGTCAGTGTGAACTCCTCTCTTTATCTCATCTGATCCCAATTAATGTTTCCAGCCTTG 929  
QY 2956 TCAACCCCTCTCTCTTACCCCACTCTGTACAGCTGGCACTGCAACAGATGCTCTAAG 3015  
Db 930 TCAGCCCTCTGTTCTCTGCCCCGCTGTCT-----CAGATATTCTTAAG 974  
QY 3016 CATAGACTTCAGGATTCATTCCTGCGAATACCTTCTGATCTCTCTCAACACAGCGC 3075  
Db 975 CACAGACCCAGGCAATTTGTTCCCTGCAAAATACCTTCCGATCTCTCTCAGACACAGCGC 1034  
QY 3076 AAGTTTCTCTACAAATTCACAGAACTGTCTGAAACAAAGACTCAGATPAACTTTCC 3135  
Db 1035 AAGTTTCTCTACAAATTCACAGAACTGTCTGAAACAAAGACTCAGATPAACTTTCC 1094  
QY 3136 CCAGTCTTTACTCAGTCAAGACCTTTGCCCTCCAGTAAACATACACAGGCCAAAGCCATCT 3195  
Db 1095 CCAGTCTTTACTCAGTCAAGACCCCACTCCAGTAAACATACACAGGCCAAAGCCATCT 1154  
QY 3196 AGACCTACCCAGGTAAATCAGATTAACAGGAGATCCCTCAAAATATAGATGACATTT 3255  
Db 1155 CCAGCCGTTTCCGGGAGTAAAGCAAACTAGGGGACGCCCAAAAGATAGATGACATTT 1214  
QY 3256 GATCTGAAACAGTAGTTTCAAAATCTGATGACAGCTTTGGCTGTAGCAGCAATAGTAGTAAT 3315  
Db 1215 GATCTGGGAGTGTCTTCCAGGTGTGACGACACTTTGGCGGGCGGCAACAGTGGCAAC 1274  
QY 3316 GCTGTTATACCCAGTACAGACAGTGTTCACCCAGTAGAGGAGAAATGCGATTAGAT 3375  
Db 1275 GCGGTATACCCAGGACAGACAGTGTTCACCGCGGTGGAGGACAGTGCAGGTAGAT 1334  
QY 3376 GTCAATACAGAGCTCAACTCCAGTATTGAGGACCTTCTTGAAGCATCTATGCTTCAAGT 3435

Db 1335 GTGAACACCGAGCTCAACTCCAGCATCGAGGACCTTCTTGAAGCATCCATGCTTCAAGT 1394  
QY 3436 GATAACAAGTAACTTTTAAAGTCAGAAGTTGCTGCTCTCTCTCTGAAAGGCTGAAAT 3495  
Db 1395 GACACACAGTCACTTTTAAAGTCCGAAAGTCCGCTCTCTCTCCGAAAGGCTGAAAT 1454  
QY 3496 GATGATACCTACAAAGATGATGTGAATCATATCAAAAGTCAAAAGAGAGATGGAAGCT 3555  
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QY 3556 GAAGAAAGAGAGCTTTAGCAATTTGCCATGGCAATGTACGCTCTCAGATGCCCTCCCC 3615  
Db 1515 GAAGAGAGAGAGCTTTAGCGATCGCATGGCGATGTACGCTCTCAGATGCCCTCCCC 1574  
QY 3616 ATAGTTCTTCAGCTGAGCTGTGAATTTGAAATGGAAGATATCATCATATTCTCAACAGGATACA 3675  
Db 1575 ATGCTCCCTCAGCTGCGGTGGAATTTGGAAGATATTTATCATTTTCAACAGGACACA 1634  
QY 3676 CCAGAGACTTACCAGGACATACCAAGCAAAACCGTATAGAGAGACACTGAATGG 3735  
Db 1635 CCAGAAACTCTTCCAGGACATACCAAGCGAAACAGCTTTACAGAGAACGCTGAGTGG 1694  
QY 3736 CTGAAGAGTCAACAGATGAGCTTGGAGCATTTTCTCTGTTATCAGGCTCAAGATGG 3795  
Db 1695 CTGAAGAGGCGCAGAGATAGGCTTCGAGCATTTTCTCTGTTACCGACACAGATGG 1754  
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QY 3856 CAAGAAAGTAGTAGAAGCACTAGAGAGAGATTAAGATGATGAGCCATCTGAATCAT 3915  
Db 1815 CAGGAGGAGTGTGGAAGCGTTGAGGAAAGAGATCCGGATGATGGTCACTTCAACCAT 1874  
QY 3916 CCAACATCATTTAGGATGTTGGAGCCAGCTGTGAGAGAGCAATTAATCTTCTCAT 3975  
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QY 3976 GAATGATGGCAGGGGATCGGTGGCTCATTTGCTGAGTAAATATGAGGCTTCAAGAA 4035  
Db 1935 GAGTGGATGGCGGAGGATCTGTGGCTCACCTTTGAGTAAATACGAGCTTTCAAGGAG 1994  
QY 4036 TCAGTAGTTTATTAACTACACTGAACTGAACTGCTCCGTGGCTTCTGATCTCCATGAAAC 4095  
Db 1995 TCAGTGTCTATTAACTACACTGAGCAGTTTACTGGTGGCTTCTCTATCTCCACGAGAAC 2054  
QY 4096 CAATCATTTACAGAGATGTCAAAGTGCCTAATTTGCTAATTTGAAGCACTGGTCAAGA 4155  
Db 2055 CAGATCATTTACAGAGACGCTCAAAGTGCCTAATTTGCTAATTTGAAGCACTGGTCAAGA 2114  
QY 4156 CTAAAGATTCAGATTTTGGAGCTGCGAGCGAGCTTGGCATCAAAAGGAACTGGTGCAGGA 4215  
Db 2115 CTGAGAAATTCAGACTTTTGGAGCTGCTGCGAGCTTGGCATCAAAAGGAACTGGTGCAGGA 2174  
QY 4216 GAGTTTCAGGACAAATTAATGGGGAACAATTTGATTTATGGCACCTGAGTACTAAGAGGT 4275  
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QY 4276 CAACAGTATGGAAGGAGCTGTGATGATGAGGTGTTGGCTGCTAATTTAGAAATGGCT 4335  
Db 2235 CAGCAGTATGTTAGGAGCTGTGATGATGAGGTGTTGGCTGCTAATTTAGAAATGGCT 2294  
QY 4336 TGTGCAAAACCCATCGGAATGCAAGAAACACTCAATCATCTTCTGTTGATTTAAG 4395  
Db 2295 TGTGCAAAACCCATCGGAATGCAAGAAACACTCAATCATCTCGCTTGTATTTAAG 2354  
QY 4396 ATTTGCTAGTCAACTACTGCTCCATCGATCCCTTCACTTTGCTCTCTGTTTACAGAT 4455  
Db 2355 ATTTGCTAGCCAACTACTGACCGTCCATCCCTGACACTGTTCCCGGCTGTCGCGAC 2414  
QY 4456 GTGGCTTCTGTTTGTAGAACTTCAACCTTCAGGACAGACCTCCATCAAGAGAGCTACTG 4515  
Db 2415 GTGGCGGTGCGCTTAGAACTTCAAGCTTCAGGCTCAGGACCGGCTCCGTCCAGAGAGCTGCTG 2474

QY 4516 AAGATCCAGTCTTTTCGTACTACATGGTAGCCAAATTATGCGATCAACTCAGTAGAAAC 4575  
DB 2475 AAACATCCGCTCTTCGTACACAGTGGTAGTAAATTTCAGATCAGCTCTAATGAGAC 2534  
QY 4576 AGGATGCTCAACAAGAGAAAAAACTTG- - - - TGGGAACCAATGATATTTCTACTGG 4631  
DB 2535 AGGATATCAACCGGAGAGAGAAAGAACTTTGTTGGCGACCATGCGCTAACCGCAG 2594  
QY 4632 CCATGATGCACCTGAACAGCTATGAACGAGGCGCAGTGGGGAACCCCTTACCTAAGTATG 4691  
DB 2595 CCTCAGCCATGTAACAGCCAGAAACCGGGCCAGCGGGAA- CCGTACCTAAGCATGTG 2653  
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DB 2654 ATTGACAAATCATGACCTGTAAGTCTAGTATGCA- AAGCCCAAACTAGTGCAGAA 2713  
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DB 2714 ACTGACACCGTGGCTTTCAGAGACTGGCTCTGGGACCAAGGAGCGGATGGGTTTG 2773  
QY 4811 CATGACTAAATGCAAGACATAATTTTATTTTGGAGCACTTTTTCAGCAA 4864  
DB 2774 CATGACTAAAGAACAGACATAAATTTA- - - - TTTTGGAGCACTTTTTCAGCTA 2825

RESULT 9

US-08-461-145C-1  
; Sequence 1, Application US/08461145C  
; Patent No. 6074861  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, GARY L.  
; TITLE OF INVENTION: NOVEL MEKK PROTEINS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lahive and Cockfield, LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,145C  
; FILING DATE: 5-JUNE-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/049,254  
; FILING DATE: 11-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/323,460  
; FILING DATE: 14-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/11690  
; FILING DATE: 14-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/04178  
; FILING DATE: 15-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/354,516  
; FILING DATE: 21-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kara, Catherine J.  
; REGISTRATION NUMBER: P-41,106  
; REFERENCE/DOCKET NUMBER: CPI-004CN1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3260 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MEKK  
STRAIN: murine  
IMMEDIATE SOURCE:  
LIBRARY: mouse liver  
CLONE: MEKK cDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..485  
NAME/KEY: CDS  
LOCATION: 486..2501  
NAME/KEY: 3'UTR  
LOCATION: 2502..3260

US-08-461-145C-1

Query Match 37.3%; Score 1955.6; DB 3; Length 3260;  
Best Local Similarity 82.7%; Pred. No. 0;  
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

QY 1996 TATACTCTTGGCCACAGTTTAGCGGAAGAAGAACTTCAAACTTCAGAGACTTCTCCAGCCAGTT 2055  
DB 1 TACTACTCTTGGCCACAGTTTAGCGGAAGAAGAACTTCAAACTTCAGAGACTTCTCCAGCCAGTT 60  
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DB 61 GTAGACACTATCTTGTCAAGTGTGCAGAT-CCACAGCGCCAGAGTCACTGTCCATA 119  
QY 2116 TCAACTGTGTGAACCTGTGCAAGCCGCAAGAGAGTTCGCAGTTCGCAGAGAAATA 2175  
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QY 2176 CTAAAGCTGGATCCCATTTGGTATTGGTGGTGTGATTGTCTTAAATTTGATTCTTGA 2235  
DB 180 CTTAAGCTGGTCCATCGGGTGTGTTGTTGATTGTCTTAAATTTGATTCTTGA 239  
QY 2236 AACCAACTGAATCAAACTTGGCAAGAACTTCTTGGCGGCTTGTCTTATAGATAGA 2295  
DB 240 AACCAAGCTGAATCAAACTTGGCAAGAACTTCTTGGCGGCTTGTCTTATAGACAG 239  
QY 2296 CTGTTGTGGAATTTCTCTGCTGAATTTTATCTCTCATATTTGTCTAGTACTGATGTTTCA 2355  
DB 300 TTGCTGTGGAATTTCTCTGCTGAATTTTATCTCTCATATTTGTCTAGTACTGATGTTTCA 359  
QY 2356 GCTGAGCTCTTGAATCAGGTATAGAGAGTCTGCTCCCTCTTAACTTTGCTTTCAG 2415  
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QY 2416 TCCATTGATAATTTCCCACTCAATGGTTGGCAAACTTTCCAGAGAGTCTACTTGAAGTCT 2475  
DB 420 TCCATTGCAATTTCCCACTCGATGGTTGGCAAGCTCTCTCGAGAGATATATCTGAGCTCT 479  
QY 2476 GCAAGAAATGTTTACTACAGTACCCCAATGTTTGTAAAACTGTAGAAATGCTGAGTGT 2535  
DB 480 GCCAGGATGGTACCGCAGTCCCGCTGTGTTTTCGAAGCTGTGTAACCACTGCTTAATGCT 539  
QY 2536 TCCAGTTCCACTCACTTCCAGAGATGCTGCGCGGTTTGTGTTGCTTATGTCAGATGAGTG 2595  
DB 540 TCTGGCTCCACCACTTCCAGAGATGCGCGCGGCTTGTGTTGCTATCGCGGATGAGTTA 599  
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DB 600 GAAATTCGGAAGCTCATCCAGTTCGGCGGTAGAGACACTTTGGATGCTCAACAGGACAGC 658  
QY 2656 TTCTTGGAGGCACTCTGTTTCCCAACACTATCTGGAACCAACAGAGAACTTCCCTCGAG 2715

Db 659 --CTTACAGCGCGTGGCCCCCACCAGCTGTCT-----AGAAAAACAGCTCCCTTGAG 707  
QY 2716 TGCACAGTCCATTTAGAGAAACTGGAAAGGATATGTGCTCAAAATTTAGTGCCAGT 2775  
Db 708 CACACAGTCCATAGAGAGAACTGGAAAGGACTAAGTGTCTACGACCTGAGTGCCAGC 767  
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QY 2836 ACA 2895  
Db 820 -----CAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 872  
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Db 873 AGTCAGTGTGTAATCT 929  
QY 2956 TCAACCCCT 3015  
Db 930 TCAGGCCCT 974  
QY 3016 CATAGACTTCAGGATTCATTTCCCTGCGAATACCTTTCTGATCTCTCTCAAAACACAGCGC 3075  
Db 975 CACAGACCCAGGATTTGTTCCCTGCGAATACCTTTCCGATCTCTCTCAGACACAGCGC 1034  
QY 3076 AAGTTCTCTACAAATCCACAGAACTGTCTCTCAAAACAAGACTCAGATAAATTTCC 3135  
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QY 3136 CCAGTCTTTACTCAGTCAAGACCTTGGCCCTCCAGTAACATACACAGCCCAAGCCATCT 3195  
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QY 3256 GATCTGAACAGTAGTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCAATAGTAGTAAT 3315  
Db 1215 GATCTGGCGAGTCTTCAGGTGTGACGACAGCTTTGGCGCGCGGCACAGTGGCAAC 1274  
QY 3316 GCTGTATACCCAGTGCAGACAGTGTTCACCCAGTAGAGAGAAATGACAGATTAGAT 3375  
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QY 3376 GTCAATACAGAGCTCAACTCCAGTATTCAGGACCTTCTTGAAGCATCTATGSCCTTCAAGT 3435  
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RESULT 10

RESOLUTION  
US-08-628-829-1

Sequence 1, Application US/08628829A

; Patent No. 6333170

GENERAL INFORMATION:

APPLICANT: Johnson, Gary L.

**TITLE OF INVENTION:** Method And Product For Regulating Cell Responsiveness To External

; FILE REFERENCE: CPI-004DVCP3

; CURRENT APPLICATION NUMBER: US/08/628,829A

CURRENT FILING DATE: 1996-04-05

CURRENT FILING DATE: 1998-04-03  
; EARLIER APPLICATION NUMBER: 08/440,421

EARLIER FILING DATE: 1995-05-15  
EARLIER AFFILIATION NUMBER: 0067

EARLIER FIDING DATE: 1993-03-13  
: EARLIER APPLICATION NUMBER: 08/323,460

EARLIER FILING DATE: 1994-10-14

; EARLIER APPLICATION NUMBER: 08/049,254

EARLIER FILING DATE: 1993-05-15

EARLIER APPLICATION NUMBER: 08/410,602

EARLIER FILING DATE: 1995-04-24

EARLIER FILING DATE: 1993-04-24  
EARLIER APPLICATION NUMBER: 08/472,934

EARLIER FILING DATE: 1995-06-06

EARLIER FILING DATE: 1993-01-01  
NUMBER OF SEO ID NOS: 25

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; SOFWAKE: Fd
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: LENGTH: 3260

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LENGTH: 3  
TYPE: DNA

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ORGANISM:  
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; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (486) (2501)

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LOCATION: (TTS-08-628-829-1

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Query Match 37.3%; Score 133.6; DB 4; Length 3200;  
Best Local Similarity 82.7%; Pred. No. 0;

Best local similarity 82.1%; Fied: NO: 0;  
Matches 2376: Conservative 0: Mismatches

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## RESULT 11

US-09-016-434-794  
; Sequence 794, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 794:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 226 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: HNT2NOT01  
; CLONE: 493684  
; US-09-016-434-794

Query Match 4.3%; Score 226; DB 4; Length 226;  
Best Local Similarity 100.0%; Pred. No. 2.2e-45;  
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 20, Application US/09371338  
; Patent No. 6613959  
; GENERAL INFORMATION:  
; APPLICANT: Sheen, Jen  
; APPLICANT: Kovtun, Yelena V.  
; APPLICANT: Chiu, Wan-Ling  
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A MAPKKK  
; TITLE OF INVENTION: PROTEIN KINASE DOMAIN  
; FILE REFERENCE: 00786/366002  
; CURRENT APPLICATION NUMBER: US/09/371,338  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 60/095,938  
; PRIOR FILING DATE: 1998-08-10  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 2527  
; TYPE: DNA  
; ORGANISM: Nicotiana tabacum  
US-09-371-338-20  
Query Match 2.3%; Score 120.4; DB 4; Length 2527;  
Best Local Similarity 50.8%; Pred. No. 3.9e-19;  
Matches 407; Conservative 0; Mismatches 376; Indels 21; Gaps 4;  
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; Sequence 14, Application US/09371338  
; Patent No. 6613959  
; GENERAL INFORMATION:  
; APPLICANT: Sheen, Jen  
; APPLICANT: Kovtun, Yelena V.  
; APPLICANT: Chiu, Wan-Ling  
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A MAPKKK  
; TITLE OF INVENTION: PROTEIN KINASE DOMAIN  
; FILE REFERENCE: 00786/366002  
; CURRENT APPLICATION NUMBER: US/09/371,338  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 60/095,938  
; PRIOR FILING DATE: 1998-08-10  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 804  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-371-338-14  
Query Match 2.2%; Score 117.2; DB 4; Length 804;  
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Search completed: May 15, 2004, 04:19:45  
Job time : 336 secs



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PI Bandman O, Thornton M, Khan FA, Walla NK, Nguyen DB, Elliott VS,  
XX Xu Y, Lu Y, Hafalia AJA, Yao MG, Gandhi AR, Arvizu C, Forsythe I;  
DR WPI; 2002-519665/55.  
DR P-PSDB; RAE25086.  
XX Novel human kinase and phosphatase polypeptide, useful in diagnosis,  
PI prevention or treatment of cardiovascular, immune system, neurological,  
PT growth, developmental, lipid and cell proliferative disorders.  
XX Claim 81; Page 202-203; 219pp; English.  
XX The present invention relates to novel human kinase and phosphatase (KAP)  
CC proteins and polynucleotides encoding such proteins. Sequences of the  
CC invention are useful for treating or preventing disorders associated with  
CC aberrant expression of KAP where the disorders include cardiovascular  
CC disorders (e.g., atherosclerosis, hypertension, vasculitis), immune  
CC system disorders (e.g., acquired immunodeficiency syndrome (AIDS), gout,  
CC anaemia, asthma, diabetes mellitus, multiple sclerosis), neurological  
CC disorders (e.g., epilepsy, stroke, Alzheimer's disease, Huntington's  
CC disease, Parkinson's disease), growth and developmental disorders (e.g.,  
CC cirrhosis, hepatitis, prolatias), lipid disorders (e.g., fatty liver,  
CC Gaucher's disease, obesity) and cell proliferative disorders (e.g.,  
CC arteriosclerosis, myelofibrosis and cancer). They are useful for drug  
CC screening techniques and to analyse the proteome of a tissue or cell  
CC type. KAP sequences are useful for creating knock-in humanised animals or  
CC transgenic animals to model human diseases, in somatic or germline gene  
CC therapy, to generate a transcript image of a tissue or cell type, for  
CC detecting differences in the chromosomal location due to inversion, or  
CC translocation among normal, carrier or affected individuals and as  
CC hybridisation probes for mapping naturally occurring genomic sequences.  
XX The present sequence is human KAP-6 cDNA

Sequence 4858 BP; 1374 A; 1140 C; 1192 G; 1152 T; 0 U; 0 Other;

Query Match 90.5%; Score 4744.8; DB 6; Length 4858;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 4793; Conservative 0; Mismatches 22; Indels 5; Gaps 3;

7 ATGGGGCGGGCGGGGAAATCGCGCTCGTCTGGGATTCCTGGGGCGGAGGCTACG 66  
1 ATGGGGCGGGCGGGGAAATCGCGCTCGTCTGGGATTCCTGGGGCGGAGGCTACG 60  
67 AGCCCTGAGGAGGCGGGCGGGAGAGCCCTCAAGGGAGGAGCGCGCGCGGCTGCC 126  
61 AGCCCTGAGGAGGCGGGCGGGAGAGCCCTCAAGGGAGGAGCGCGCGGCGGCTGCC 120  
127 GCGGGAAGTCTGCGGGAGGCGGGCGAGCGGGGGCGGCGAGCGGGCGGCGGCGG 186  
121 GCGGGAAGTCTGCGGGAGGCGGGCGAGCGGGGGCGGCGAGCGGGCGGCGGCGG 180  
187 CAGCTCGGCAAGTGGGAGTGGAGCTGGACCTGGAACCTGCTGAGCGCGCTCTTCCTT 246  
181 CAGCTCGCAAGTGGGAGTGGAGCTGGACCTGGAACCTGCTGAGCGCGCTCTTCCTT 240  
247 GCGGCTCACCGCGGCTCTTCGACTTCCCGGTCGCGGAGCGCGGCGGCGGCGGCGG 306  
241 GCGGCTCACCGCGGCTCTTCGACTTCCCGGTCGCGGAGCGCGGCGGCGGCGGCGG 300  
307 AGTGGAGACGGCTTCAGCGCTGTTGGGCTGCGCGCGCGCGCGCGCGCGCGCGCGG 366  
301 AGTGGAGACGGCTTCAGCGCTGTTGGGCTGCGCGCGCGCGCGCGCGCGCGCGCGG 360  
367 GCGGCGCCACCTTACCGAGTGGTGGGCGGCGGAGCGGGCGGCTTCGAGTCCCGGCGG 426  
361 GCGGCGCCACCTTACCGAGTGGTGGGCGGCGGAGCGGGCGGCTTCGAGTCCCGGCGG 420  
427 GCGGAGCGCGGAGAGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 486  
421 GCGGAGCGCGGAGAGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 480

487 GGTCTGTGAGATGGAGATAAAGAAACTCTCAAAGGTTTGCAACAAGATGATGATCGTCCA 546  
481 GGTCTGTGAGATGGAGATAAAGAAACTCTCAAAGGTTTGCAACAAGATGATGATCGTCCA 540  
547 GAGGAACGAATGATCAGGAGAAACTGAAGCAACCTGTATGCCAGCTCGAAGCAGAA 606  
541 GAGGAACGAATGATCAGGAGAAACTGAAGCAACCTGTATGCCAGCTCGAAGCAGAA 600  
607 TGGTTGGAAGAGAGAAATAGCGAGGGCTGTGGTGGTAAACCAATCCCAAGTTAAAGGA 666  
601 TGGTTGGAAGAGAGAAATAGCGAGGGCTGTGGTGGTAAACCAATCCCAAGTTAAAGGA 660  
667 GATGANTCTGAATGAATCACTTAGCAGCTGAGTCTCCAGAGAGGTCAGGCAAGTCGG 726  
661 GATGANTCTGAATGAATCACTTAGCAGCTGAGTCTCCAGAGAGGTCAGGCAAGTCGG 720  
727 GCTTACCAAGCTTCCAAAGGGCCGACGAGTCTCTCTCTGGCAACTCCCAATCAGGTGCG 786  
721 GCTTACCAAGCTTCCAAAGGGCCGACGAGTCTCTCTCTGGCAACTCCCAATCAGGTGCG 780  
787 ACAGTGAATCAAGATCTCCAGAGATGAGGAGAAAGAGTTTCCCAAGTGGCTTTTTCAG 846  
781 ACAGTGAATCAAGATCTCCAGAGATGAGGAGAAAGAGTTTCCCAAGTGGCTTTTTCAG 840  
847 AGTGGCAGAAATCACACCCCGAAGAGCCCTTCCAGAGAGGCTTCTCACCATATAGC 906  
841 AGTGGCAGAAATCACACCCCGAAGAGCCCTTCCAGAGAGGCTTCTCACCATATAGC 900  
907 CCGTGAAGAAACAAACCGCGCTGTTTAAAGTGTGCGGGCCAGACTGTACTTACTGCGAG 966  
901 CCGTGAAGAAACAAACCGCGCTGTTTAAAGTGTGCGGGCCAGACTGTACTTACTGCGAG 960  
967 CAGATAGGCGCTAACTCTTCTGATTTGGAGAGAGCAGCCAGACAATAAATACCGGGTG 1026  
961 CAGATAGGCGCTAACTCTTCTGATTTGGAGAGAGCAGCCAGACAATAAATACCGGGTG 1020  
1027 TTTTATTTGGGCTCAGAACTGCGAGCTGTGCACTGTGGAACATTTCTGTATTCTATCTGCTATT 1086  
1021 TTTTATTTGGGCTCAGAACTGCGAGCTGTGCACTGTGGAACATTTCTGTATTCTATCTGCTATT 1080  
1087 GTGATGCTCGGGTGTTCACACTAGAACCTTCAGACCCCAATGTTATGGAAGAAACCTTTA 1146  
1081 GTGATGCTCGGGTGTTCACACTAGAACCTTCAGACCCCAATGTTATGGAAGAAACCTTTA 1140  
1147 AAGAAATTTTGTGAGTTGAGAGTTTGTTCAGAAATATCAAGTAGGGCTGAGTCAAGGATC 1206  
1141 AAGAAATTTTGTGAGTTGAGAGTTTGTTCAGAAATATCAAGTAGGGCTGAGTCAAGGATC 1200  
1207 AAGCTCCATCTCGTAACACCCATCCAGAGATTTTGTTCAGCATGTCAAATTTCTCATACA 1266  
1201 AAGCTCCATCTCGTAACACCCATCCAGAGATTTTGTTCAGCATGTCAAATTTCTCATACA 1260  
1267 TTGTTCATCATCTAGTACTTCTACGTCTAGTTCAGAAACAGCATAAAGGATGAAGAGAA 1326  
1261 TTGTTCATCATCTAGTACTTCTACGTCTAGTTCAGAAACAGCATAAAGGATGAAGAGAA 1320  
1327 CAGATGCTCTATTGCTTTGTTGGCATGCTGTGAGAGAGAGTCTTACAGTGTGTGAA 1386  
1321 CAGATGCTCTATTGCTTTGTTGGCATGCTGTGAGAGAGAGTCTTACAGTGTGTGAA 1380  
1387 GACGGCTGCAAGAAACAGCTGCAACCACTGCACTGATGTCAAATTTGGGCGAAGAGTGTAGA 1446  
1381 GACGGCTGCAAGAAACAGCTGCAACCACTGCACTGATGTCAAATTTGGGCGAAGAGTGTAGA 1440  
1447 AGAAATAGAGAACCTTTAATATGTCCTCTTGTAGATCTAAGTGGAGATCTCATGATTTTC 1506  
1441 AGAAATAGAGAACCTTTAATATGTCCTCTTGTAGATCTAAGTGGAGATCTCATGATTTTC 1500  
1507 TACAGCCACAGATGTCAGAGTCTCTGTGGATTTCCCTTTCTTCCCTCAGAGCTGCACAGCAG 1566  
1501 TACAGCCACAGATGTCAGAGTCTCTGTGGATTTCCCTTTCTTCCCTCAGAGCTGCACAGCAG 1560  
1567 CAACCCGTAACAGAGAGCGCTTTGGCTGGATCAGAAAGGATCAAGAGAGCAATTTTAAAC 1626

1561 CAAACCGTACAGCAGCAGCCTTTGGCTGGATCAGGAAGAAATCAAGAGAGCAATTTTAAAC 1620  
1627 CTTACTCATTTATGGAAGTACGAAATCCCTCCCTGCTTTACAAAGATTTAGCTGAGCCATGG 1686  
1621 CTTACTCATTTATGGAATCAGCAAAATCCCTCCCTGCTTTACAAAGATTTAGCTGAGCCATGG 1680  
1687 ATTCAAGTGTGTTGGAATGGAACCTGTTGGCTGCTTTATTTCTAGAAACTGGAATGTGAGA 1746  
1681 ATTCAAGTGTGTTGGAATGGAACCTGTTGGCTGCTTTATTTCTAGAAACTGGAATGTGAGA 1740  
1747 GAGATGCCCTCAGGCGTCTTTCCCATGATGTAGTGGGCGCTGCTGTTGGCAATGGG 1806  
1741 GAGATGCCCTCAGGCGTCTTTCCCATGATGTAGTGGGCGCTGCTGTTGGCAATGGG 1800  
1807 GAGAGCACTGGAATTTCTGGGGCAGCAGTGGAGAGCCGCGAGTGGGGAGCCACCAAGT 1866  
1801 GAGAGCACTGGAATTTCTGGGGCAGCAGTGGAGAGCCGCGAGTGGGGAGCCACCAAGT 1860  
1867 GGGTCTTCCAGACAGCATGATCTAGGAGATGTGGTGAGGCATGCTGCAGCGTTCGTCA 1926  
1861 GGGTCTTCCAGACAGCATGATCTAGGAGATGTGGTGAGGCATGCTGCAGCGTTCGTCA 1920  
1927 ATGCTGTGCTGACCCCTGCTACAAAGTGTACGTTGCTGCTTTAAAAACATTTGAGAGCC 1986  
1921 ATGCTGTGCTGACCCCTGCTACAAAGTGTACGTTGCTGCTTTAAAAACATTTGAGAGCC 1980  
1987 ATGCTGTGATATACCTCTGCGACAGTTTACGGAAGAAAGATCAAACTTCAGAGACTTCTC 2046  
1981 ATGCTGTGATATACCTCTGCGACAGTTTACGGAAGAAAGATCAAACTTCAGAGACTTCTC 2040  
2047 CAGCCAGTGTGAGACACATCTAGTCAATGTGCAGATGCCAATGCCCAACAGTCAG 2106  
2041 CAGCCAGTGTGAGACACATCTAGTCAATGTGCAGATGCCAATGCCCAACAGTCAG 2100  
2107 CTGTCCATATCAACACTGTTGGAATCTGTGCAAGGCCAAGCAGAGAGTTGGCAGTTGGC 2166  
2101 CTGTCCATATCAACACTGTTGGAATCTGTGCAAGGCCAAGCAGAGAGTTGGCAGTTGGC 2160  
2167 AGAGAAATCTAAAGCTGGATCATTGGTATGCTGATGATGATGCTTAAATGT 2226  
2161 AGAGAAATCTAAAGCTGGATCATTGGTATGCTGATGATGATGCTTAAATGT 2220  
2227 ATCTTGGAAACCAAACTGAAATCAAACTGGAAGAACTTCTTGCCGCCCTTTGCTTT 2286  
2221 ATCTTGGAAACCAAACTGAAATCAAACTGGAAGAACTTCTTGCCGCCCTTTGCTTT 2280  
2287 ATAGATAGACTGTTGTTGGAATTTCTGCTGAATTTTATCCTCATATGTCAGTACTGAT 2346  
2281 ATAGATAGACTGTTGTTGGAATTTCTGCTGAATTTTATCCTCATATGTCAGTACTGAT 2340  
2347 GTTTCACAAGCTGAGCCCTGTTGAAATCAGGTATAGAGAGCTGCTGCTCCCTCTTAACTTT 2406  
2341 GTTTCACAAGCTGAGCCCTGTTGAAATCAGGTATAGAGAGCTGCTGCTCCCTCTTAACTTT 2400  
2407 GCTTTGAGTCCATGTGATTAATCCCATCTCAATGTTGGCAAACTTTCGAGAGATCTAC 2466  
2401 GCTTTGAGTCCATGTGATTAATTTCCCACTCAATGTTGGCAAACTTTCGAGAGATCTAC 2460  
2467 TTGAGTCTCGAAGAAATGTTTACTACAGTACCCCATGTTTTCAAAACCTGTTAGAAATG 2526  
2461 TTGAGTCTCGAAGAAATGTTTACTACAGTACCCCATGTTTTCAAAACCTGTTAGAAATG 2520  
2527 CTGAGTGTGTTCAAGTTCACATCAATCCAGGATGCGTGCCTGTTGATGGCTATTGCA 2586  
2521 CTGAGTGTGTTCAAGTTCACATCAATCCAGGATGCGTGCCTGTTGATGGCTATTGCA 2580  
2587 GATGAGTGGAAATTTGCCGAAGCCATCCAGTTGGCGGTAGAGACACTTTTGGATGGTCAA 2646  
2581 GATGAGTGGAAATTTGCCGAAGCCATCCAGTTGGCGGTAGAGACACTTTTGGATGGTCAA 2640  
2647 CAGGACAGCTTCTTCAGGCGATCTGTTCCCAACCACTATCTGGAACCCACAGAGAACAGT 2706

2641 CAGGACAGCTTCTTCAGGCGATCTGTTCCCAACAACATATCTGGAACCCACAGAGAACAGT 2700  
2707 TCCCTGAGTGCACAGTCCATTTTAGAGAAAACCTGGAAAAGGATTTATGTGCTTACAAAATTG 2766  
2701 TCCCTGAGTGCACATCCATTTAGAGAAAACCTGGAAAAGGATTTATGTGCTTACAAAATTG 2760  
2767 AGTGCCAGTTTCAAGAGCAATTTCTGAGAGACTGGCCGACATTTTCAATGAGACCTTCTAGT 2826  
2761 AGTGCCAGTTTCAAGAGCAATTTCTGAGAGACTGGCCGACATTTTCAATGAGACCTTCTAGT 2820  
2827 TCACAAACAAACAAACAAACAAACAGAGCAACCAAGCCCAATGGTTTCAAAACAAAGGC 2886  
2821 T----CAACAAACAAACAAACAAACAGAGCAACCAAGCCCAATGGTTTCAAAACAAAGGC 2877  
2887 AGACCCCAAGTGTGTTGAACT 2946  
2878 AGACCCCAAGTGTGTTGAACT 2937  
2947 CCAGCCTTGTCAACCCCTTCT 3006  
2938 CCAGCCTTGTCAACCCCTTCT 2997  
3007 GTCTCTAAGCATAGACTTTTCAAGGATTCATTCCTGCAAGATPACCTTTGTGATCTCTCTCAA 3066  
2998 GTCTCTAAGCATAGACTTTTCAAGGATTCATTCCTGCAAGATPACCTTTGTGATCTCTCTCAA 3057  
3067 ACACAGCCGAGTGTCTCTCAATTTCCACAGAACTGTCTCTGAAAACAAAGACTTCAGAT 3126  
3058 ACACAGCCGAGTGTCTCTCAATTTCCACAGAACTGTCTCTGAAAACAAAGACTTCAGAT 3117  
3127 AAACCTTTCCTCCAGTCTTACTCAGTCAAGACCTTTGCCCTCCAGTAAACATACACAGGCCA 3186  
3118 AAACCTTTCCTCCAGTCTTACTCAGTCAAGACCTTTGCCCTCCAGTAAACATACACAGGCCA 3177  
3187 AAGCCATCTAGACTTACCCGAGTAAATACAGTAAACAGGGAGATCCCTCTCAAAAATAGC 3246  
3178 AAGCCATCTGAGACTTACCCGAGTAAATACAGTAAACAGGGAGATCCCTCTCAAAAATAGC 3237  
3247 ATGACACTTGTATCTCAACAGTAGTTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCAAT 3306  
3238 ATGACACTTGTATCTGAACAGTAGTTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCAAT 3297  
3307 AGTAGTAAATGCTGTTATACCCGAGTGCACAGACAGTGTTCACCCGAGTACAGGAGAAATGC 3366  
3298 AGTAGTAAATGCTGTTATACCCGAGTGCACAGACAGTGTTCACCCGAGTACAGGAGAAATGC 3357  
3367 AGATTAGATGTCATACAGAGCTCAATCTCCAGTATTTAGGACCTTCTTTGAAGCATCTATG 3426  
3358 AGATTAGATGTCATACAGAGCTCAATCTCCAGTATTTAGGACCTTCTTTGAAGCATCTATG 3417  
3427 CTTTCAAGTGATACAAAGTAACTTTTAAAGTCAGAAAGTGTGCTGCTCTCTCTCTCTCTCTCT 3486  
3418 CTTTCAAGTGATACAAAGTAACTTTTAAAGTCAGAAAGTGTGCTGCTCTCTCTCTCTCTCTCT 3477  
3487 GCTGAAAATGATGATACCTTACAAAGATGATGTAATCATATCAAAAAGTCAAGAGAGAG 3546  
3478 GCTGAAAATGATGATACCTTACAAAGATGATGTAATCATATCAAAAAGTCAAGAGAGAG 3537  
3547 ATGGAAGCTGAAAGAGAGAGCTTTAGCAATTTGCAATGGCAATGTACAGCGTCTCAGGAT 3606  
3538 ATGGAAGCTGAAAGAGAGAGCTTTAGCAATTTGCAATGGCAATGTACAGCGTCTCAGGAT 3597  
3607 GCTCTCCCATAGTCTCTCAGCTGAGGTTGAAAATGGAGAGATATCATCATTTATTCAA 3666  
3598 GCTCTCCCATAGTCTCTCAGCTGAGGTTGAAAATGGAGAGATATCATCATTTATTCAA 3657  
3667 CAGGATACACAGAGACTCTTACAGGACATACCAAGCAAAAACACCGTATAGAGAGAC 3726  
3658 CAGGATACACAGAGACTCTTACAGGACATACCAAGCAAAAACACCGTATAGAGAGAC 3717  
3727 ACTGAATGCTGAAAGGTCAAAGATAGGCTTTGGAGCAATTTCTCTGTTTATCAGGCT 3786  
3718 ACTGAATGCTGAAAGGTCAAAGATAGGCTTTGGAGCAATTTCTCTGTTTATCAGGCT 3777



of the invention has cardiant, antiarteriosclerotic, hypotensive, immunosuppressive, dermatological, anorectic, cyrostatic, antidiabetic, haemostatic, anti-HIV, antischismatic, antibacterial, virucide, neuroprotective, nootropic, antiparkinsonian, and antilipaemic activity. A polynucleotide encoding a polypeptide of the invention may have a use in gene therapy, and as a vaccine. A polypeptide of the invention is useful in the manufacture of a medicament for treating a syndrome associated with a human disease, the disease selected from a pathology associated with the polypeptide. These may also be used in diagnosing, treating or preventing NOVX-associated disorders such as cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes, haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease, multiple sclerosis, infections, anorexia, cancer-associated cachexia, neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's disease), haematopoietic disorders, dyslipidaemias and other wasting disorders associated with chronic diseases. The nucleic acids are also used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. The present sequence encodes a NOVX polypeptide of the invention.

SQ Sequence 4840 BP; 1357 A; 1154 C; 1196 G; 1133 T; 0 U; 0 Other;

Query Match 90.3%; Score 4737.8; DB 9; Length 4840;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 4771; Conservative 0; Mismatches 12; Indels 6; Gaps 2;

QY	1	GAGAAATGGCGCGCGCGGGAATCGCGCTCGTCGCGGATTCGCGGCGCCAGG	60
DB	55	GAGAAATGGCGCGCGCGGGAATCGCGCTCGTCGCGGATTCGCGGCGCCAGG	114
QY	61	GCTAGAGCCCTGAGCGAGCGCGCGGAGAGCCCTCAAGCGGAGGAGCGCGCGCG	120
DB	115	GCTAGAGCCCTGAG---CAGCGCGCGGAGAGGCGCCCTCAAGCGGAGGAGCGCGCGCG	171
QY	121	GCTGCGCGGCGACTGCTCGGAGCGCGGCGGAGCGCGGCGCGCGCGCGCGCG	177
DB	172	GCTGCGCGGCGACTGCTCGGAGCGCGGCGGAGCGCGGCGCGCGCGCGCGCG	231
QY	178	CGGCGCGCGCGAGTGGGAAAGTGGGAGTGGGAGCTGGACAGCTGCTGAGCAGCG	237
DB	232	CGGCGCGCGCGAGTGGGAAAGTGGGAGTGGGAGCTGGACAGCTGCTGAGCAGCG	291
QY	238	CTCTTCTTCCGCGCTCACCGCGCGCTCTCGACTTCCCGCTCGCGGAGCGCGCGGAC	297
DB	292	CTCTTCTTCCGCGCTCACCGCGCGCTCTCGACTTCCCGCTCGCGGAGCGCGCGGAC	351
QY	298	GCAGCGGAGTGGGAGCGCGCTTCCAGCTGCGGCGCGCGCGCGCGCGCGCGCGCG	357
DB	352	GCAGCGGAGTGGGAGCGCGCTTCCAGCTGCGGCGCGCGCGCGCGCGCGCGCGCG	411
QY	358	AGCGCGCGCGCGCGCGCTTCCAGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG	417
DB	412	AGCGCGCGCGCGCGCGCTTCCAGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG	471
QY	418	CCGCGAGCG	477
DB	472	CCGCGAGCG	531
QY	478	GCCTCCGCGCGCTGAGTGGGAGTAAAGAACTCTCAAGGGTTCACAGATGGAT	537
DB	532	GCCTCCGCGCGCTGAGTGGGAGTAAAGAACTCTCAAGGGTTCACAGATGGAT	591
QY	538	GATCGTCCAGGAGAAAGTATGATGAGGAGAACTCAAGGCAACCTGTATGCCAGCTGG	597
DB	592	GATCGTCCAGGAGAAAGTATGATGAGGAGAACTCAAGGCAACCTGTATGCCAGCTGG	651
QY	598	AAGCAGGAATGGTGGAAAGAGAAATAGCGAGCGCGCTGTGTTAAACCAATCCCA	657
DB	652	AAGCAGGAATGGTGGAAAGAGAAATAGCGAGCGCGCTGTGTTAAACCAATCCCA	711
QY	658	GTTAAAGGAGATGGAATCAATCACTTAGCAGCTGAGCTCCAGGAGAGCTCCAG	717

DB	712	GTTAAAGGAGATGGAATCAATCACTTAGCAGCTGAGCTCCAGGAGAGGTCCAG	771
QY	718	GCAAGTGGCGCTTCCAGCTTCCAAAGCGCGAGCTGCTCTCTCTGGGCACTCCCA	777
DB	772	GCAAGTGGCGCTTCCAGCTTCCAAAGCGCGAGCTGCTCTCTCTGGGCACTCCCA	831
QY	778	TCAGGTGCGCAGTGAATTCAGAACTCTCCAGAGTAAGGAGAAAAAGAGTTTCCCAGTG	837
DB	832	TCAGGTGCGCAGTGAATTCAGAACTCTCCAGAGTAAGGAGAAAAAGAGTTTCCCAGTG	891
QY	838	CTTTTTCAGAGTGGCGAGTACACACCCCGGAGAGCCCTTCCAGAGTGGCTTCTCA	897
DB	892	CTTTTTCAGAGTGGCGAGTACACACCCCGGAGAGCCCTTCCAGAGTGGCTTCTCA	951
QY	898	CCATATAGCCCTGAGGAAACAAACCGCGCTGTTAAACAAAGTATCGGCGCAGCTGAC	957
DB	952	CCATATAGCCCTGAGGAAACAAACCGCGCTGTTAAACAAAGTATCGGCGCAGCTGAC	1011
QY	958	TTACTCAGAGATAGGCGCTAACTCTTCTCTGATGAGGAGAGAGCCCGACAAATAA	1017
DB	1012	TTACTCAGAGATAGGCGCTAACTCTTCTCTGATGAGGAGAGAGCCCGACAAATAA	1071
QY	1018	TACCGGCTGTTATTGGGCTCAGAACTGCACTGCACTGCGGAACTTCTGTATTCAT	1077
DB	1072	TACCGGCTGTTATTGGGCTCAGAACTGCACTGCACTGCGGAACTTCTGTATTCAT	1131
QY	1078	CTGCTATTTGTGATGCTCGGCTGTTTCAACTAGAACCTTTCAGACCAATGTTATGAGA	1137
DB	1132	CTGCTATTTGTGATGCTCGGCTGTTTCAACTAGAACCTTTCAGACCAATGTTATGAGA	1191
QY	1138	AAAACTTTAAAGAAATTTGAGGTTGAGAGTTTGTCCAGAAATATCACTAGTAGGCTAGC	1197
DB	1192	AAAACTTTAAAGAAATTTGAGGTTGAGAGTTTGTCCAGAAATATCACTAGTAGGCTAGC	1251
QY	1198	TCAGGATCAAGCTCCATCTCGTAAACATCCAGAGTTTGTTCAGCGATGTCAAT	1257
DB	1252	TCAGGATCAAGCTCCATCTCGTAAACATCCAGAGTTTGTTCAGCGATGTCAAT	1311
QY	1258	TCTCATACATGTCATCTACTACTCTAGCTGATGTTTCAAGAAACAGCAATAAGGAT	1317
DB	1312	TCTCATACATGTCATCTACTACTCTAGCTGATGTTTCAAGAAACAGCAATAAGGAT	1371
QY	1318	GAAGAGAAACAGATGTCTATTTGCTTGTGGGATGCTTGTATGAAGAAAGTCTTACA	1377
DB	1372	GAAGAGAAACAGATGTCTATTTGCTTGTGGGATGCTTGTATGAAGAAAGTCTTACA	1431
QY	1378	GTGTGTGAGACCGCTGCGAGGACCACTGCACTGCACTGCAATTTGGGCGAGAA	1437
DB	1432	GTGTGTGAGACCGCTGCGAGGACCACTGCACTGCACTGCAATTTGGGCGAGAA	1491
QY	1438	GAGTGTAGAAAGAAATAGAGAACTTTAATATGTCCCTTTGTAGATCTAAGTGAGATCT	1497
DB	1492	GAGTGTAGAAAGAAATAGAGAACTTTAATATGTCCCTTTGTAGATCTAAGTGAGATCT	1551
QY	1498	CATGATTTTCAGCGCACGATGTTCAAGTCTGTGGATTCCTCTTCCCTCAGAGCT	1557
DB	1552	CATGATTTTCAGCGCACGATGTTCAAGTCTGTGGATTCCTCTTCCCTCAGAGCT	1611
QY	1558	GCACAGCAGCAAAACCGTTACAGCAGCAGCTTTTGGCTGGATCAGAAAGGAATCAAGAGC	1617
DB	1612	GCACAGCAGCAAAACCGTTACAGCAGCAGCTTTTGGCTGGATCAGAAAGGAATCAAGAGC	1671
QY	1618	AATTTTAACTTACTCATTTATGGAATCAGAAATCCCTCTCTCTTACAAAGATTTAGCT	1677
DB	1672	AATTTTAACTTACTCATTTATGGAATCAGAAATCCCTCTCTCTTACAAAGATTTAGCT	1731
QY	1678	GAGCATGGATTCAGGTTGTTGGAATCGTGGCTGCTTATTTTCTAGAAACTGG	1737
DB	1732	GAGCATGGATTCAGGTTGTTGGAATCGTGGCTGCTTATTTTCTAGAAACTGG	1791
QY	1738	AATGTGAGAGATGCGGCTCAGCGCTTTTCCATGATGTCAGTGGGCGCTGCTGTTG	1797
DB	1792	AATGTGAGAGATGCGGCTCAGCGCTTTTCCATGATGTCAGTGGGCGCTGCTGTTG	1851



QY 1798 GCAATGGGAGAGACCTGGAAATTTCTGGGGGAGCAGTGGAGCAGCCCGAGTGGGGG 1857  
DB 1852 GCAATGGGAGAGACCTGGAAATTTCTGGGGGAGCAGTGGAGCAGCCCGAGTGGGGG 1911  
QY 1858 GCGACCAAGTGGGCTCTCCAGACAGATATCTCAGAGATGTFGGAGGCACTGCTGAGC 1917  
DB 1912 GCCACCAAGTGGGCTCTCCAGACAGATATCTCAGAGATGTFGGAGGCACTGCTGAGC 1971  
QY 1918 GTTCTGCAATGGTCTGCTGAGCCCTGCTPACAAAGTGTACGTTGCTGCTTTAAAAACA 1977  
DB 1972 GTTCTGCAATGGTCTGCTGAGCCCTGCTPACAAAGTGTACGTTGCTGCTTTAAAAACA 2031  
QY 1978 TTGAGAGCCATGCTGGTATATCTCTTGGCCACAGTTTGTAGCGGAAAGATCAAACTTCAG 2037  
DB 2032 TTGAGAGCCATGCTGGTATATCTCTTGGCCACAGTTTGTAGCGGAAAGATCAAACTTCAG 2091  
QY 2038 AGACTTTCACAGCAGTGTGTAGACACCACTCTAGTCAAACTGTGCAGATGCCAATAGCCGC 2097  
DB 2092 AGACTTTCACAGCAGTGTGTAGACACCACTCTAGTCAAACTGTGCAGATGCCAATAGCCGC 2151  
QY 2098 ACAAGTCAGTGTCCATATCAACACTGTGTGAACCTGTGCAAGGCCAAGCAGAGAGTTG 2157  
DB 2152 ACAAGTCAGTGTCCATATCAACACTGTGTGAACCTGTGCAAGGCCAAGCAGAGAGTTG 2211  
QY 2158 GCAGTTGCAGAGAAATCTAAAGCTGGATCCATTTGGTATTTGGTGTGTTGATTATGTC 2217  
DB 2212 GCAGTTGCAGAGAAATCTAAAGCTGGATCCATTTGGTATTTGGTGTGTTGATTATGTC 2271  
QY 2218 TTAATTTGTAATCTTTGGAACCAAACTGAAATCAAACTGAAATTTGTCGCGC 2277  
DB 2272 TTAATTTGTAATCTTTGGAACCAAACTGAAATCAAACTGAAATTTGTCGCGC 2331  
QY 2278 CTTTGTCTATAGATAGCTGTGTGGAATTTCTGCTGATTTTATCTCATATTTGTC 2337  
DB 2332 CTTTGTCTATAGATAGCTGTGTGGAATTTCTGCTGATTTTATCTCATATTTGTC 2391  
QY 2338 AGTACTGATGTTTCAACAGCTGAGCCTGTGAAATCAGGTATAGAAAGCTGCTGCTCCCTC 2397  
DB 2392 AGTACTGATGTTTCAACAGCTGAGCCTGTGAAATCAGGTATAGAAAGCTGCTGCTCCCTC 2451  
QY 2398 TTAACCTTTGCTTTGCACTGATGATTAATTTCCCACTCAATGTTGCAAACTTTCCAGA 2457  
DB 2452 TTAACCTTTGCTTTGCACTGATGATTAATTTCCCACTCAATGTTGCAAACTTTCCAGA 2511  
QY 2458 AGGATCTACTTCAAGTCTGCAAGAAATGTTACTACAGTACCCCATGTTGTTTCAAACTG 2517  
DB 2512 AGGATCTACTTCAAGTCTGCAAGAAATGTTACTACAGTACCCCATGTTGTTTCAAACTG 2571  
QY 2518 TTAGAAATGCTGAGTGTTCAGTTCGACTCACTTACAGGATGCGTGCCTGTTGATG 2577  
DB 2572 TTAGAAATGCTGAGTGTTCAGTTCGACTCACTTACAGGATGCGTGCCTGTTGATG 2631  
QY 2578 GCTATTGCAGATGAGTGGAAATTTGCCGAAGCCATCCAGTTGGCGGTAGAGACACTTTG 2637  
DB 2632 GCTATTGCAGATGAGTGGAAATTTGCCGAAGCCATCCAGTTGGCGGTAGAGACACTTTG 2691  
QY 2638 GATGTCACAGGACAGCTTCTTGAGCGCATCTGTTTCCCAACAACATCTTGGAAACCA 2697  
DB 2692 GATGTCACAGGACAGCTTCTTGAGCGCATCTGTTTCCCAACAACATCTTGGAAACCA 2751  
QY 2698 GAGAACAGTTCCTGAGTGCACAGTCCATTTAGAGAAACCTGGAAGAGATATGCT 2757  
DB 2752 GAGAACAGTTCCTGAGTGCACAGTCCATTTAGAGAAACCTGGAAGAGATATGCT 2811  
QY 2758 ACAAATTTGAGTGCAGGACATTTCTGAGAGACTGGCCAGCATTTTCAGTAGGA 2817  
DB 2812 ACAAATTTGAGTGCAGGACATTTCTGAGAGACTGGCCAGCATTTTCAGTAGGA 2871  
QY 2818 CTTTCTAGTTCACAAAC 2877  
DB 2872 CTTTCTAGTTCACAAAC 2931

QY 2878 ACAAAGGAGAGACCCCAAGCTGTTTGAACCTCTCTCTTTATCTCATCTTTCCAA 2937  
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QY 2938 TTAATGTTTCAAGCCTTGTCAACCCCTTCTTCTTCTACCCCATCTGTACAGCTGGCACT 2997  
DB 2992 TTAATGTTTCAAGCCTTGTCAACCCCTTCTTCTTCTACCCCATCTGTACAGCTGGCACT 3051  
QY 2998 GCACAGATGCTCTTAAGCATAGACTTCAGGGATTCATTCTCTGCAGAAATACCTTCTGCA 3057  
DB 3052 GCACAGATGCTCTTAAGCATAGACTTCAGGGATTCATTCTCTGCAGAAATACCTTCTGCA 3111  
QY 3058 TCTCTCTAAACACAGCGGCAAGTTTCTCTCAATTCACAGAACTGTCTCTGAAACAAA 3117  
DB 3112 TCTCTCTAAACACAGCGGCAAGTTTCTCTCAATTCACAGAACTGTCTCTGAAACAAA 3171  
QY 3118 GACTCAGATTAATTTTCCCCAGTCTTTACTCAGTCAAGACCTTGCCTCCAGTAAACATA 3177  
DB 3172 GACTCAGATTAATTTTCCCCAGTCTTTACTCAGTCAAGACCTTGCCTCCAGTAAACATA 3231  
QY 3178 CACAGGCCAAAGCCATCTAGACCTTACCOCAGGTAAATACAAGTAAACAGGGAGATCCCTCA 3237  
DB 3232 CACAGGCCAAAGCCATCTAGACCTTACCOCAGGTAAATACAAGTAAACAGGGAGATCCCTCA 3291  
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DB 3292 AAAAATAGCATGACACTTGTATCTGAACAGTGTCCAAATGTGATGACAGCTTTGGCTGT 3351  
QY 3298 AGCAGCAATPAGTAAAGTGTATATCCAGTGCAGACAGTGTTCACCCAGTAGAG 3357  
DB 3352 AGCAGCAATPAGTAAAGTGTATATCCAGTGCAGACAGTGTTCACCCAGTAGAG 3411  
QY 3358 GAGAAATCAGATTAAGTGTCAATACAGAGCTCAACTCCAGTATTGAGAGCTTTCTTCAA 3417  
DB 3412 GAGAAATCAGATTAAGTGTCAATACAGAGCTCAACTCCAGTATTGAGAGCTTTCTTCAA 3471  
QY 3418 GCATCTATGCTTCAAGTGATAACAACAGTAACTTTTAAAGTCAAGAGTGTCTCTGTCT 3477  
DB 3472 GCATCTATGCTTCAAGTGATAACAACAGTAACTTTTAAAGTCAAGAGTGTCTCTGTCT 3531  
QY 3478 CTTGAAAGGCTGAAATGATGATACCTACAAAGATGATGAAATCAATAAACAAGTGC 3537  
DB 3532 CTTGAAAGGCTGAAATGATGATACCTACAAAGATGATGAAATCAATAAACAAGTGC 3591  
QY 3538 AAGAGAGATGGAAGCTGAAGAGAGAGAGCTTTAGCAATTTGCCATGCGCAATGTCAOG 3597  
DB 3592 AAGAGAGATGGAAGCTGAAGAGAGAGAGCTTTAGCAATTTGCCATGCGCAATGTCAOG 3651  
QY 3598 TCTCAGATGCTTCCCATAGTTCCTCAGCTGAGGTTGAAATGGAGAGATATCATC 3657  
DB 3652 TCTCAGATGCTTCCCATAGTTCCTCAGCTGAGGTTGAAATGGAGAGATATCATC 3711  
QY 3658 ATTATTCAACAGGATACACAGAGACTCTACAGGACATACCAAGCAACCAACCGTAT 3717  
DB 3712 ATTATTCAACAGGATACACAGAGACTCTACAGGACATACCAAGCAACCAACCGTAT 3771  
QY 3718 AGAAGAGACACTGAATGCTGAAAGTCAACAGATAGGCTTGGAGCAATTTCTTCTTGT 3777  
DB 3772 AGAAGAGACACTGAATGCTGAAAGTCAACAGATAGGCTTGGAGCAATTTCTTCTTGT 3831  
QY 3778 TATCAGGCTCAAGATGTGGAACTGAACTTTAATGGCTGTAAACAGGTGACTTATGTC 3837  
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QY 4078 TCGTATCTCCATGAAGAAACCAATCATTTACAGAGATGTCAAAGAGTGCCAAATTTGCTAAT 4137
Db 4132 TCGTATCTCCATGAAGAAACCAATCATTTACAGAGATGTCAAAGAGTGCCAAATTTGCTAAT 4191
QY 4138 GACAGACTGTGTCAGAGACTAAGAAATGCAAGTTTGGAGCTGCAGCCAGTTGGCATCA 4197
Db 4192 GACAGACTGTGTCAGAGACTAAGAAATGCAAGTTTGGAGCTGCAGCCAGTTGGCATCA 4251
QY 4198 AAGGAACTGTGTCAGAGAGTTTCAGGACACAATTTACTGGGACAAATTCATTTATGSCA 4257
Db 4252 AAGGAACTGTGTCAGAGAGTTTCAGGACANAATTTACTGGGACANAATTTGCAATTTATGSCA 4311
QY 4258 COTGAGGTACTAAGAGGTCAACAGTATGGAAGGAGCTGTGATGTATGGAGTGTGGCTGT 4317
Db 4312 COTGAGGTACTAAGAGGTCAACAGTATGGAAGGAGCTGTGATGTATGGAGTGTGGCTGT 4371
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Db 4372 GCTATTATAGAAATGGCTGTGCAAAACCAACCATGGAATGCAAAACCAATTCACATCAT 4431
QY 4378 CTGTCTTTGATATTTAAGATTCTAGTCAACTACTGTCTCATCGATCCCTTTCATTTG 4437
Db 4432 CTGTCTTTGATATTTAAGATTCTAGTCAACTACTGTCTCATCGATCCCTTTCATTTG 4491
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QY 4558 ATCACTACAGTAGAAGAGAGTGTCTCAACAGAGAAAGAACTTTGGGGAAACCAT 4617
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Db 4732 TACCTAAGTATGTGATTGCAAAATCATGATCTGTACCTAAGCTCAGTATGCAAAAGCCCA 4791
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Db 4792 AACTAGTGAGAACTGTAAACTGTGCCTTTCAAAGAACTGGCCCTAGG 4840
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## RESULT 3

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AAF27079
ID AAF27079 standard; DNA; 4693 BP.
XX
AC AAF27079;
XX
DT 06-APR-2001 (first entry)
XX
DE Human MEK1 cdna.
XX
KW Human MEK1; mitogen-activated protein kinase kinase kinase 1;
KW MEK kinase 1; MAP/ERK kinase kinase 1; pro-apoptotic;
KW apoptosis signal regulation; programmed cell death;
KW serine/threonine kinase; MAP kinase cascade; JNK/SAPK;
KW Jun N-terminal kinase/stress-activated protein kinase; JNK/SAPK;
KW NF-kappa-B-mediated transcription regulation; expression inhibition;
KW antisense therapy; hyperproliferative disorder; cancer; inflammation; ss.
```

```
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FT mat_peptide 1..4485
FT /*tag= a
FT /product= "Human MEK1"
XX
XX US6168950-B1.
XX
XX 02-JAN-2001.
XX
XX 23-JUL-1999; 99US-00359756.
XX
XX 23-JUL-1999; 99US-00359756.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Cowseert LM, Gaarde W, Ward DT;
XX
XX WPI; 2001-122264/13.
XX
XX P-PSDB; AAB60291.
XX
XX New antisense compound targeting nucleic acid encoding human mitogen-
XX activated protein kinase 1 (MEK1), useful for treating diseases
XX or conditions associated with MEK1 expression, or preventing
XX inflammation or tumor formation.
XX
XX Claim 1; Col 42-54; 35pp; English.
XX
XX This sequence represents human MEK1 cdna. MEK1 (also known as mitogen-
XX activated protein kinase kinase 1, MEK kinase 1 and MAP/ERK kinase
XX kinase 1) is a dual-specific serine/threonine kinase which mediates
XX cellular responses to mitogenic stimuli, being involved in JNK/SAPK (Jun
XX N-terminal kinase/stress-activated protein kinase) MAP kinase cascades.
XX MEK1 regulates signalling events associated with apoptosis (programmed
XX cell death) and NF-kappa-B, both of which have been associated with the
XX development of hyperproliferative disorders such as cancer. Specifically,
XX MEK1 lies directly downstream of Bcl-2 in an apoptotic signalling
XX cascade, and plays a critical role in the control of NF-kappa-B-mediated
XX transcription at multiple points in the apoptotic cascade. The invention
XX relates to antisense oligonucleotides targeted to the human MEK1 gene,
XX which inhibit its expression. A series of oligonucleotides (AAF27086-
XX AAF27125) were designed to target different regions of the human MEK1
XX RNA, and were analysed for their effect on MEK1 mRNA levels by
XX quantitative real-time PCR. The oligonucleotides of the invention are
XX useful for diagnosis, prevention and treatment of conditions associated
XX with MEK1 expression, such as inflammation, and cancer and other
XX hyperproliferative disorders
```

SQ Sequence 4693 BP; 1340 A; 1102 C; 1143 G; 1108 T; 0 U; 0 Other;

Query Match 87.0%; Score 4564.6; DB 4; Length 4693;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 4647; Conservative 0; Mismatches 39; Indels 9; Gaps 5;

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QY 65 CGAGCCCTGAGGCGGCGGCGGAGGAGCCCTCAAGGCGAGCAGCGCCCGCGGCTG 124
Db 2 CGAGCCCTGAGGCGGCGGCGGAGGAGCCCTCAAGGCGAGCAGCGCGCGGCTG 61
QY 125 CCGCGGAGCTGCTGCGGAGGCGGCGGAGCGCGGCGGCGGAGCGGAGCGGCGGCG 184
Db 62 CCGCGGAGCTGCTGCGGAGGCGGCGGAGCGGCGGCGGAGCGGAGCGGCGGCG 121
QY 185 GGAGAGCTGCCAAAGTGGAGGTGGAGCTGACACAGCTGCTGTAGAGCCGCTCTTCC 244
Db 122 GGCAGCTGCCAAAGTGGAGGTGGAGCTGACACAGCTGCTGTAGAGCCGCTCTTCC 181
QY 245 TTGCGGCTCACCGCGGCTCTCTCGACTTCCCGTGGCGGAGCCCGGAGCGGAGCGG 304
Db 182 TTGCGGCTCACCGCGGCTCTCTCGACTTCCCGTGGCGGAGCCCGGAGCGGAGCGG 241
QY 305 GGAGTGGGACCGGCTCCAGCCCTGTGGCGGTGGCGGCGGCGGCGGCGGAGCGGCGG 364
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Db 302 GCGGCGCCACCTTACCAGTCTGGTGGCGGCGCGGACAGCGGCGCCTCGAGTCCCGCAG 361  
Qy 425 GCGGCGGACCGCGGAGAGCGGCGCGCGCGCGCGCGCGCTCTCTGCGAGCGCGCCCG 484  
Db 362 GCGGCGGACCGCGGAGAGCGGCGCGCGCGCGCGCGCGCTCTCTGCGAGCGCGCCCG 421  
Qy 485 CCGGTGCTGAGATGAGAAATAAGAAATCTCAAAGGTTGCAACAAGATGATGATGTC 544  
Db 422 CCGGTGCTGAGATGAGAAATAAGAAATCTCAAAGGTTGCAACAAGATGATGATGTC 481  
Qy 545 CAGAGAAAGAAATGATCAGGAGAAATGAGAGCAACTGATGCGCAGCCTGGAAGCAGC 604  
Db 482 CAGAGAAAGAAATGATCAGGAGAAATGAGAGCAACTGATGCGCAGCCTGGAAGCAGC 541  
Qy 605 AATGTTGGAAAGGAGAAATAGGCGAGGCGCTGTGGTAAATCCCAATCCCACTTAAAG 664  
Db 542 AATGTTGGAAAGGAGAAATAGGCGAGGCGCTGTGGTAAATCCCAATCCCACTTAAAG 601  
Qy 665 GAGATGAGATCTGAATGAATCACTTAGCAGCTGAGTCTCCAGGAGAGTCCAGGCAAGTG 724  
Db 602 GAGATGAGATCTGAATGAATCACTTAGCAGCTGAGTCTCCAGGAGAGTCCAGGCAAGTG 661  
Qy 725 CGGCTTCCAGCTTCCAAAGCCGACGAGCTCTCTCTGCGCAACTCCCACTCAGGTC 784  
Db 662 CGGCTTCCAGCTTCCAAAGCCGACGAGCTCTCTCTGCGCAACTCCCACTCAGGTC 721  
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Db 842 GCGCTGAGAAACAAACCGCGTGTAAACAAGTATGCGGCGCAGCTGACTTACTGTC 901  
Qy 965 AGCAGATAGGCGCTTAACCTTTCTCTGATTGGAGGAGACAGCCAGACAAATAAACCGG 1024  
Db 902 AGCAGATAGGCGCTTAACCTTTCTCTGATTGGAGGAGACAGCCAGACAAATAAACCGG 961  
Qy 1025 TGTATTATGGGCTCAGAACTGACGCTGACGCTGGAAACATCTGATATCATCTGCTAT 1084  
Db 962 TGTATTATGGGCTCAGAACTGACGCTGACGCTGGAAACATCTGATATCATCTGCTAT 1021  
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Db 1022 TTGTGATGCTCGGGTGTTCACCTAGAACCTTCAGACCCCAATGTTATGGAGAAACCTT 1081  
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Db 1082 TAAAGATTTTGAAGTGTAGAGTTTGTTCAGAAATATCACAGTAGGCGTAGCTCAAGGA 1141  
Qy 1205 TCAAGCTCCATCTGCTAACACCATCCAGAGTTTGTTCAGCATGTCAAATCTCATATA 1264  
Db 1142 TCAAGCTCCATCTGCTAACACCATCCAGAGTTTGTTCAGCATGTCAAATCTCATATA 1201  
Qy 1265 CATTFGTCATCTAGTACTTCTAGCTGATGTCAGAAACAGCATAAAGGATGAAGAGG 1324  
Db 1202 CATTFGTCATCTAGTACTTCTAGCTGATGTCAGAAACAGCATAAAGGATGAAGAGG 1261  
Qy 1325 AACAGATGTCCTATTCTGTTGGGATCTGTTGAGAGAGAGTCTTACAGTGTGTG 1384  
Db 1262 AACAGATGTCCTATTCTGTTGGGATCTGTTGAGAGAGAGTCTTACAGTGTGTG 1321  
Qy 1385 AAGACGGCTGCAGGAAACAGCTGCACCACTGATGTCATTTGGGCGAGAGAGTGA 1444

Db 1322 AAGACGGCTGCAGGAAACAGCTGCACCACTGCATGTCATTTGGGCGAGAGAGTGA 1381  
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Db 1382 GAAGAAATAGAGAACTTTAATATATGTCCCTTTGTAGATCTAAGTGGAGATCTCATGAT 1441  
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Qy 1565 AGCAAAACCGTACAGAGCAGCCTTTGGCTGGATCAAGAGGAATCAAGAGCAATTTTA 1624  
Db 1502 AGCAAAACCGTACAGAGCAGCCTTTGGCTGGATCAAGAGGAATCAAGAGCAATTTTA 1561  
Qy 1625 ACCTTACTCATTTATGAACTCAGCAAAATCCCTCTCTGTACAAAGATTTAGTGAAGCAT 1684  
Db 1562 ACCTTACTCATTTATGAACTCAGCAAAATCCCTCTCTGTACAAAGATTTAGTGAAGCAT 1621  
Qy 1685 GATTCAGTGTGTGAATGGAATCTGTTGGCTGCTTATTTCTTAGAAATCGGAATGTGA 1744  
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Qy 1925 CAATGTGTGTGTGACCTGTCTACAAAGTGTACGTTGCTGCTTTAAAAACATTGAGAG 1984  
Db 1862 CAATGTGTGTGTGACCTGTCTACAAAGTGTACGTTGCTGCTTTAAAAACATTGAGAG 1921  
Qy 1985 CAATGTGTGTATATCTCTGCGCAGTTTACGAGTGGAAAGATCAAACTTCAGAGACTTC 2044  
Db 1922 CAATGTGTGTATATCTCTGCGCAGTTTACGAGTGGAAAGATCAAACTTCAGAGACTTC 1981  
Qy 2045 TCCAGCAGTGTGTAGACCACTCTTAGTCAAAATGTGCAAGATGCCAATAGCCGCAAGTTC 2104  
Db 1982 TCCAGCAGTGTGTAGACCACTCTTAGTCAAAATGTGCAAGATGCCAATAGCCGCAAGTTC 2041  
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DB 2882 TAAATGTTTCAGCCTTGTCAACCCCTTCTCTCTACCCCATCTGTACAGCTGGCACTG 2941  
QY 2999 CAACAGATGTCTTAAGCATAGACTTCAGGATTCATTCCTCTGAGAACTACCTCTGCAT 3058  
DB 2942 CAACAGATGTCTTAAGCATAGACTTCAGGATTCATTCCTCTGAGAACTACCTCTGCAT 3001  
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DB 3002 CTCCTCAAAACAGCGCAAGTTCCTPACAAATCCACAGAACTGCTGAAAACAAAG 3061  
QY 3119 ACTCAGATAAATTTCCCGAGTCTTACTCAGTCAAGACCTTGCCCTCCAGTAACATAC 3178  
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QY 3779 ATCAGGCTCAAGATGTTGGAACTTTAATCGCTGTTTAAACAGGTCATTTATGTCA 3838  
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QY 3839 GAAACAATCTTTCTGAGCAAGAGAGTAGTAGAGCACTAAGAGAAAGATATGAATGA 3898  
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DB 3842 TGAGCCATCTGAATCATCCAAACATCATTAGATGTTGGAGCCACGTTGAGAGAGCA 3901  
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DB 3902 ATTACAATCTCTTCAATGGAATGGATGGCAGGGGGATCGGTGCTCATTTGCTGAGTAAT 3961  
QY 4019 ATGGAGCCTTCAAGNAATCAGTAGTNTAATCTACACTGAAACAGTTCCTCGGCGCTTT 4078  
DB 3962 ATGGAGCCTTCAAGNAATCAGTAGTNTAATCTACACTGAAACAGTTCCTCGGCGCTTT 4021  
QY 4079 CGTATCTCCATGAAAACCAATCATTACAGAGATGTCAAAGGTGCCAATTTGCTAATTTG 4138  
DB 4022 CGTATCTCCATGAAAACCAATCATTACAGAGATGTCAAAGGTGCCAATTTGCTAATTTG 4081  
QY 4139 ACAGCACTGCTCAGAGACTAAGAAATTCAGATTTTGGAGCTTCAGCCAGGTTGGCATCAA 4198  
DB 4082 ACAGCACTGCTCAGAGACTAAGAAATTCAGATTTTGGAGCTTCAGCCAGGTTGGCATCAA 4141  
QY 4199 AAGGAATCTGCTCAGAGAGTTCAGGGGCAATTAATCTGGGCAATTTGCAATTTATGGCAC 4258  
DB 4142 AAGGAATCTGCTCAGAGAGTTCAGGGGCAATTAATCTGGGCAATTTGCAATTTATGGCAC 4201  
QY 4259 CTGAGTATCAAGAGTCAACAGTATGGAAGAGCTGTGATGTATGAGTGTGCTGTG 4318  
DB 4202 CTGAGTATCAAGAGTCAACAGTATGGAAGAGCTGTGATGTATGAGTGTGCTGTG 4261  
QY 4319 CTATTTAGAAATGGCTTCTGCAAAACCAACCATGGAATGCAAGAAAACACTCCAATCATC 4378  
DB 4262 CTATTTAGAAATGGCTTCTGCAAAACCAACCATGGAATGCAAGAAAACACTCCAATCATC 4321  
QY 4379 TTGCTTTGATATTTAAGATTGCTAGTGCACACTGCTCCATCGATCCCTTCAATTTGT 4438  
DB 4322 TTGCTTTGATATTTAAGATTGCTAGTGCACACTGCTCCATCGATCCCTTCAATTTGT 4381  
QY 4439 CTCTGTTTACAGATGCTGCTCTTCTGTTGTTTGAACCTTCAACTCAGGACAGACCTC 4498  
DB 4382 CTCTGTTTACAGATGCTGCTCTTCTGTTGTTTGAACCTTCAACTCAGGACAGACCTC 4441  
QY 4499 CATCAAGAGAGCTTACTGAAAGCATCCAGTCTTTCGTAATATGTTGCAATTTATGCA 4558  
DB 4442 CATCAAGAGAGCTTACTGAAAGCATCCAGTCTTTCGTAATATGTTGCAATTTATGCA 4501  
QY 4559 TGAACCTACAGTAGAAGAGTGTCTCAACAGAGAAAACAACTTGTGGGAGACCACTT 4618  
DB 4502 TGAACCTACAGTAGAAGAGTGTCTCAACAGAGAAAACAACTTGTGGGAGACCACTT 4560  
QY 4619 GATATTTACTGTCATGATGCTGCACTGAAACAGCTATGAAACGAGCCAGTGGGAAACCTT 4678  
DB 4561 GATAT--CTACGCCCATGATGCCACTGAAACAGCTATGAAACGAGCCAGTGGGAAACCTT 4618  
QY 4679 ACCTAAGTATGATTGACAAATCATGATCTGTACTGATCAGTATGATATGCAAAAGCCAA 4738



Db 962 TGTATTGGGCTCAGAACTGCAGCTGTGCACATGGACATTTCTGTATTTCATCTGCTAT 1021  
Qy 1085 TTGTGATGCTCGGGTGTTCACCTAGAACCTTCAGACCCOATGTTATGAGAAAAAATT 1144  
Db 1022 TTGTGATGCTCGGGTGTTCACCTAGAACCTTCAGACCCOATGTTATGAGAAAAAATT 1081  
Qy 1145 TAAAGAAATTTTGGAGTTCAGAGTGTGTTCCAGAAATATCAGTAGGCGTAGCTCAAGGA 1204  
Db 1082 TAAAGAAATTTTGGAGTTCAGAGTGTGTTCCAGAAATATCAGTAGGCGTAGCTCAAGGA 1141  
Qy 1205 TCAAGCTCCATCTCGTAAACCACTCAGAAATGTTGTTACGATGCAATCTCAAT 1264  
Db 1142 TCAAGCTCCATCTCGTAAACCACTCAGAAATGTTGTTACGATGCAATCTCAAT 1201  
Qy 1265 CATGTGATCATCTAGTACTTCTAGTCTAGTTCAGAAACAGCATAAAGATGAAGAG 1324  
Db 1202 CATGTGATCATCTAGTACTTCTAGTCTAGTTCAGAAACAGCATAAAGATGAAGAG 1261  
Qy 1325 AACGATGTGCTTATTTGCTTGTGTCATGTCATGTCATGTCATGTCATGTCATGTC 1384  
Db 1262 AACGATGTGCTTATTTGCTTGTGTCATGTCATGTCATGTCATGTCATGTCATGTC 1321  
Qy 1385 AAGACGGCTGCAGAAACAGCTGCACCACTGCATGTCATGTCATGTCATGTCATGTC 1444  
Db 1322 AAGACGGCTGCAGAAACAGCTGCACCACTGCATGTCATGTCATGTCATGTCATGTC 1381  
Qy 1445 GAAGAAATAGAAACCTTTAATATGTCCTTGTGTCATGTCATGTCATGTCATGTCAT 1504  
Db 1382 GAAGAAATAGAAACCTTTAATATGTCCTTGTGTCATGTCATGTCATGTCATGTCAT 1441  
Qy 1505 TCTACAGCAGAGTGTCAAGTCTGTCGATGTCGATGTCGATGTCGATGTCGATGTCGAT 1564  
Db 1442 TCTACAGCAGAGTGTCAAGTCTGTCGATGTCGATGTCGATGTCGATGTCGATGTCGAT 1501  
Qy 1565 AGCAAAACGTCAGCAGCAGCCTTTGGCTGTCATGTCATGTCATGTCATGTCATGTCAT 1624  
Db 1502 AGCAAAACGTCAGCAGCAGCCTTTGGCTGTCATGTCATGTCATGTCATGTCATGTCAT 1561  
Qy 1625 ACCTTACTCATATGGAATCAGCAATCCCTCTGTCATGTCATGTCATGTCATGTCATGTC 1684  
Db 1562 ACCTTACTCATATGGAATCAGCAATCCCTCTGTCATGTCATGTCATGTCATGTCATGTC 1621  
Qy 1685 GGATTCAGGTGTTGGATGGAATCGTGTGCTGCTTATTTCTAGAAACTGGAATGTGA 1744  
Db 1622 GGATTCAGGTGTTGGATGGAATCGTGTGCTGCTTATTTCTAGAACTGGAATGTGA 1681  
Qy 1745 GAGAGATGGCCCTCAGGCGCTTTCCTCATGATGTCAGTGGGCGCTCTGCTGTGGCAATG 1804  
Db 1682 GAGAGATGGCCCTCAGGCGCTTTCCTCATGATGTCAGTGGGCGCTCTGCTGTGGCAATG 1741  
Qy 1805 GGGAGAGCACTGGAAATTTCTGGGGCAGCAGTGAAGCAGCCCGAGTGGGGAGCCACCA 1864  
Db 1742 GGGAGAGCACTGGAAATTTCTGGGGCAGCAGTGAAGCAGCCCGAGTGGGGAGCCACCA 1801  
Qy 1855 GTGGTCTTCCAGACAGTATCTCAGAGATGTTGGAGGATGTTGGAGGATGTTGGAGG 1924  
Db 1802 GTGGTCTTCCAGACAGTATCTCAGAGATGTTGGAGGATGTTGGAGGATGTTGGAGG 1861  
Qy 1925 CAATGGTCTGTGCTGACCTCTCTACAAAGTGTACGTTGCTGCTTTAAACATTTGAGAG 1984  
Db 1862 CAATGGTCTGTGCTGACCTCTCTACAAAGTGTACGTTGCTGCTTTAAACATTTGAGAG 1921  
Qy 1985 CCATGCTGGTATATCTCTTTCACAGTTTAGCGGAAGAAATCAAACTTCAGAGCTTC 2044  
Db 1922 CCATGCTGGTATATCTCTTTCACAGTTTAGCGGAAGAAATCAAACTTCAGAGCTTC 1981  
Qy 2045 TCCAGCCAGTTGTAGACACCATCTAGTCAATGTGCAGATGTCATAGCGCAAGTC 2104  
Db 1982 TCCAGCCAGTTGTAGACACCATCTAGTCAATGTGCAGATGTCATAGCGCAAGTC 2041  
Qy 2105 AGCTGTCCATATCAACTGTGGAATCTGTCAAAAGCCCAAGCAGGAGAGTTGGCAGTTG 2164  
Db 2042 AGCTGTCCATATCAACTGTGGAATCTGTCAAAAGCCCAAGCAGGAGAGTTGGCAGTTG 2101

Qy 2165 GCAGAGAAATATATAAAGCTGGATCCATTTGGTATTGGTGGTGTGATATATGCTTAAAT 2224  
Db 2102 GCAGAGAAATATATAAAGCTGGATCCATTTGGTATTGGTGGTGTGATATATGCTTAAAT 2161  
Qy 2225 GTATTCTTGGAAACCAAACTGAATCAAACTAATTTGCAAGAACTTCTTGGCCGCCCTTTGTC 2284  
Db 2162 GTATTCTTGGAAACCAAACTGAATCAAACTAATTTGCAAGAACTTCTTGGCCGCCCTTTGTC 2221  
Qy 2285 TTATAGATAGACTGTGTTGGAAATTTCTGCTGGAATTTTATCTCATATTTGTCAGTACTG 2344  
Db 2222 TTATAGATAGACTGTGTTGGAAATTTCTGCTGGAATTTTATCTCATATTTGTCAGTACTG 2281  
Qy 2345 ATGTTTCAACAGCTGAGCCTGTTGAAATCAGATATAAAGAGCTGCTGCTCTTAACT 2404  
Db 2282 ATGTTTCAACAGCTGAGCCTGTTGAAATCAGATATAAAGAGCTGCTGCTCTTAACT 2341  
Qy 2405 TTGCTTTGCAAGTCCATGATTAATTTCCACTCAATGGTTGGCAAACTTTCCAGAAAGATCT 2464  
Db 2342 TTGCTTTGCAAGTCCATGATTAATTTCCACTCAATGGTTGGCAAACTTTCCAGAAAGATCT 2401  
Qy 2465 ACTTGAGTCTCAGAAATGTTTACTCAGATACCCCATGTTGTTTCAAACTGTTAGAA 2524  
Db 2402 ACTTGAGTCTCAGAAATGTTTACTCAGATACCCCATGTTGTTTCAAACTGTTAGAA 2461  
Qy 2525 TGTGAGTGTTCCTAG---TTCCACTCACTTCCAGGATGCTGCTGCGCTTTGATGGCTA 2581  
Db 2462 TGTGAGTGTTCCTAGTGTTCCTCACTTCCAGGATGCTGCTGCGCTTTGATGGCTT 2521  
Qy 2582 TTGCGATGAGTGGAAATTTCCGAGGCATCCAGTTGGGCGTAGAAGACACTTTGGATG 2641  
Db 2522 ATGCGATGAGTGGAAATTTCCGAGGCATCCAGTTGGGCGTAGAAGACACTTTTACAAC 2581  
Qy 2642 GTCAACAGGACAGC---TTCTTGCAGGCATCTGTTCCCACTACTATCTGGAACACACAGA 2699  
Db 2582 GACAAACACACACAGCTTTTGCAGGCATCTGTTCCCACTACTATCTGGAACACACAGA 2641  
Qy 2700 GAACAGTTCCCC-TGAGTGCAAGTCCATTTAGAGAAAACTGGAAGAGATATGTCCTA 2758  
Db 2642 GAACAGTTCCCCTTGAGTGCAAGTCCATTTAGAGAAAACTGGAAGAGATATGTCCTA 2701  
Qy 2759 CAAAATTTAGTCCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGCACTTTCAATGAGAC 2818  
Db 2702 CAAAATTTAGTCCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGCACTTTCAATGAGAC 2761  
Qy 2819 CTTCTAGTTCAAACACACACAAACAAACAAACAGAGAACCAAGCAATGTTCAA 2878  
Db 2762 CTTCTAGTTCAAACACACACAAACAAACAGAGAACCAAGCAATGTTCAA 2821  
Qy 2879 CAAAAGGACAGCCACAGTCAAGTGTGAACTCCTCTCTCTTATCTCATATCCCCT 2938  
Db 2822 CAAAAGGACAGCCACAGTCAAGTGTGAACTCCTCTCTCTTATCTCATATCCCCT 2881  
Qy 2939 TAATGTTTCCAGCTTGTCAACCCCTTCTTCTTCTTACCCCATCTGTACAGTGGCCTG 2998  
Db 2882 TAATGTTTCCAGCTTGTCAACCCCTTCTTCTTCTTACCCCATCTGTACAGTGGCCTG 2941  
Qy 2999 CAAAGATGCTCTAAGCATAGACTTCAAGGATTTCAATTCCTGCGAGATACCTTCTGCAT 3058  
Db 2942 CAAAGATGCTCTAAGCATAGACTTCAAGGATTTCAATTCCTGCGAGATACCTTCTGCAT 3001  
Qy 3059 CTCCTCAACACAGCGCAAGTTTCTTACAAATTTCCAGAACTGCTCTGAAAAAACAAG 3118  
Db 3002 CTCCTCAACACAGCGCAAGTTTCTTACAAATTTCCAGAACTGCTCTGAAAAAACAAG 3061  
Qy 3119 ACTCAGATAACTTTTCCCGCTTTTACTCAGTCAAGCCCTTGGCTCCAGTACATAC 3178  
Db 3062 ACTCAGATAACTTTTCCCGCTTTTACTCAGTCAAGCCCTTGGCTCCAGTACATAC 3121  
Qy 3179 ACAGGCCAAAGCCACTAGACCTACCCAGGTAATACAAAGTAAACAGGAGATCCCTCAA 3238  
Db 3122 ACAGGCCAAAGCCACTCGACCTACCCAGGTAATACAAAGTAAACAGGAGATCCCTCAA 3181

QY 3239 AAAATAGCATGACACTGTGCTGAACAGTAGTCTCCAAATGTGATGACAGCTTTGGCTGTA 3298  
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QY 3182 AAAATAGCATGACACTGTGCTGAACAGTAGTCTCCAAATGTGATGACAGCTTTGGCTGTA 3241  
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QY 3299 GCAGCAATAGTAGTAATGCTGTTATACCCAGTGCAGACAGTGTTCACCCAGTAGAGG 3358  
Db |||||  
QY 3242 GCAGCAATAGTAGTAATGCTGTTATACCCAGTGCAGACAGTGTTCACCCAGTAGAGG 3301  
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QY 3359 AGAATGAGATAGTAGTCAATACAGAGCTCAACTCCAGTATGAGGACCTTCTTGAAG 3418  
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QY 3302 AGAATGAGATAGTAGTCAATACAGAGCTCAACTCCAGTATGAGGACCTTCTTGAAG 3361  
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QY 3419 CATCTATGCCCTCAAGTGATACAAACAGTAACCTTTTAAAGTCAGAGTGTGCTGCTCTC 3478  
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QY 3362 CATCTATGCCCTCAAGTGATACAAACAGTAACCTTTTAAAGTCAGAGTGTGCTGCTCTC 3421  
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QY 3479 CTGAAGAGGCTGAAATGATGATACCTACAAAGATGATGATCATTAATCAAAAGTGCA 3538  
Db |||||  
QY 3422 CTGAAGAGGCTGAAATGATGATACCTACAAAGATGATGATCATTAATCAAAAGTGCA 3481  
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QY 3539 AAGAGAAGATGGAAGCTGAAGAAGAAAGCTTTAGCAATTTGCCATGGCAATGTCAAGCGT 3598  
Db |||||  
QY 3482 AAGAGAAGATGGAAGCTGAAGAAGAAAGCTTTAGCAATTTGCCATGGCAATGTCAAGCGT 3541  
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QY 3599 CTCAGGATGCCCTCCCATAGTCTCTCAGCTGCAGGTTGAAATGGAGAGATATCATCA 3658  
Db |||||  
QY 3542 CTCAGGATGCCCTCCCATAGTCTCTCAGCTGCAGGTTGAAATGGAGAGATATCATCA 3601  
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QY 3602 TTATTTCAACAGGATACACAGAGACTCTTACAGACATACCAAGCAAAACAAACCGTATA 3661  
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QY 3719 GAGAGACACTGAATGGCTGAAAGGTCAACAGATAGGCTTGGAGCAATTTCTCTTGTT 3778  
Db |||||  
QY 3662 GAGAGACACTGAATGGCTGAAAGGTCAACAGATAGGCTTGGAGCAATTTCTCTTGTT 3721  
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QY 3722 ATCAGGCTCAAGATGTGGAACTTGAACCTTTAATGGCTGTAAACAGGTCACTTATGCA 3781  
Db |||||  
QY 3839 GAAACACATCTTCTGAGCAAGAAAGATGATGAGCACTTAAGAGAGAGATGAATGA 3898  
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QY 3782 GAAACACATCTTCTGAGCAAGAAAGATGATGAGCACTTAAGAGAGAGATGAATGA 3841  
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QY 3842 TGAGGCACTGTAATCATCCAAACATCATTAGCATGTTGGGAGCCACGTGTGAGAGAGCA 3901  
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QY 3959 ATTACATCTCTTCAATGGAATGGATGGCAGGGGATCGTGGCTCATTTGCTGAGTAAAT 4018  
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QY 3902 ATTACATCTCTTCAATGGAATGGATGGCAGGGGATCGTGGCTCATTTGCTGAGTAAAT 3961  
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QY 3962 ATGGAGCCTTCAAGAAATCAGTAGTTATTAACTACCTGAAACAGTACTCCGTGGCCTTT 4021  
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QY 4079 COTATCTCCATGAAACCAATCATCTACAGATGTCAAAAGGTGCCAATTTGCTAATTG 4138  
Db |||||  
QY 4022 COTATCTCCATGAAACCAATCATCTACAGATGTCAAAAGGTGCCAATTTGCTAATTG 4081  
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QY 4139 ACAGCACTGGTCAGAGACTGAAGTTGAGATTTGGAGCTGCAGCCAGGTTGGCATCAA 4198  
Db |||||  
QY 4082 ACAGCACTGGTCAGAGACTGAAGTTGAGATTTGGAGCTGCAGCCAGGTTGGCATCAA 4141  
Db |||||  
QY 4199 AAGGAACCTGGTCAGAGAGGTTTCAGGACAATTACTCGGACAATTTGCAATTTATGGCAC 4258  
Db |||||  
QY 4142 AAGGAACCTGGTCAGAGAGGTTTCAGGACAATTACTCGGACAATTTGCAATTTATGGCAC 4201  
Db |||||  
QY 4259 CTGAGGTACTAGAGGTCAACAGTATGGAAGAGCTGTGATGATGGAGTCTTGGCTGTG 4318  
Db |||||  
QY 4202 CTGAGGTACTAGAGGTCAACAGTATGGAAGAGCTGTGATGATGGAGTCTTGGCTGTG 4261  
Db |||||  
QY 4319 CTATTATGAATGGCTTGTGCAAAACCAACCATGGAATGCAGAAAAACACTCCAATCATC 4378  
Db |||||

Db 4262 CTATTATGAATAATGGCTTGTGCAAAACCAACCATGGAATGCAAAAAACACTCCAATCATC 4321  
QY 4379 TTGCTTTGATATTTAAGATTGCTAGTGCAACTACTGCTCCATCGATCCCTTCAATTGT 4438  
Db 4322 TTGCTTTGATATTTAAGATTGCTAGTGCAACTACTGCTCCATCGATCCCTTCAATTGT 4381  
QY 4439 CTCCTGGTTTACGAGATGTGGCTCTTCTGTTTGTAGAACTTCAACCTCAGGACAGACCTC 4498  
Db 4382 CTCCTGGTTTACGAGATGTGGCTCTTCTGTTTGTAGAACTTCAACCTCAGGACAGACCTC 4441  
QY 4499 CATCAAGAGAGCTACTGAAGCATCCAGTCTTCTGTTCTGTACTATGTTAGCCATTTATGAGA 4558  
Db 4442 CATCAAGAGAGCTACTGAAGCATCCAGTCTTCTGTTCTGTACTATGTTAGCCATTTATACAGA 4501  
QY 4559 TCAACTCAGTAGAAGAAACAGGATGCTCAACAAGAGAAAAAACTTGTGGGAAACCAATT 4618  
Db 4502 TCAACTAC-GTAGAAACAGGATGCTCAACAAGAGAAAAAACTTGTGGGAAACCAATT 4560  
QY 4619 GATATTCTACTGGCCATGATGCCACTGAACAGCTATGAACGAGGCCAGTGGGAAACCCCTT 4678  
Db 4561 GATAT-CTACGGCCATGATGCCACTGAACAGCTATGAACGAGGCCAGTGGGAAACCCCTT 4618  
QY 4679 ACCTAAGTATGTGATTGACAAATCATGATCTGTACCTAAGCTCAGTATGCAAAAGCCCAA 4738  
Db 4619 ACCTAAGTATGTGATTGACAAATCATGATCTGTACCTAAGCTCAGTATGCAAAAGCCCAA 4678  
QY 4739 ACTAGTGCAGAACT 4753  
Db 4679 ACTAGTGCAGAACT 4693

RESULT 5  
AAS68564  
ID AAS68564 standard; cDNA; 4488 BP.  
XX  
AC AAS68564;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #4368.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI: 2001-639362/73.  
DR P-PSDB; AB004377.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensic, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 1; SEQ ID NO 4368; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,



CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIFO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 4488 BP; 1264 A; 1057 C; 1101 G; 1066 T; 0 U; 0 Other;

Query Match 83.7%; Score 4390.6; DB 5; Length 4488;  
 Best Local Similarity 99.1%; Pred. No. 0;  
 Matches 4447; Conservative 0; Mismatches 34; Indels 6; Gaps 3;

QY	65	CGAGCCCTGAGGCGGCGGCGGAGAGCCCTCAAGCGAGCAGCGCGCGCGGCTG	124
DB	2	CGAGCCCTGAGGCGGCGGCGGAGAGCCCTCAAGCGAGCAGCGCGCGGCTG	61
QY	125	CCGCGGAGCTGCTCGGAGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGG	184
DB	62	CCGCGGAGCTGCTCGGAGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGG	121
QY	185	GGCAGCTGCGCAAGTGGAGGTGTGGAGCTGGACCGAGCTGCTGAGCAGCGCTTCC	244
DB	122	GGCAGCTGCGCAAGTGGAGGTGTGGAGCTGGACCGAGCTGCTGAGCAGCGCTTCC	181
QY	245	TTGCGGCTCAGCGCGGCTCTCGACTTCCCGCTGCGCGGAGCGCGGAGCGGCGG	304
DB	182	TTGCGGCTCAGCGCGGCTCTCGACTTCCCGCTGCGCGGAGCGCGGAGCGGCGG	241
QY	305	GGAGTGGGACCGGCTTCAGCCTGTGGCGGTGCGCGGCGGCGGCGGCGGCGG	364
DB	242	GGAGTGGGACCGGCTTCAGCCTGTGGCGGTGCGCGGCGGCGGCGGCGGCGG	301
QY	365	CGGCGGCCACCTTACCGAGTCGGTGGCGGCGGCGGAGCAGCGGCGCTCGAGTCCG	424
DB	302	CGGCGGCCACCTTACCGAGTCGGTGGCGGCGGCGGAGCAGCGGCGCTCGAGTCCG	361
QY	425	CGGCGGAGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	484
DB	362	CGGCGGAGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	421
QY	485	CCGCTCGTGGATGGAGAAATAAGAACTCTCAAGGGTGGCAAGATGGATGATCGTC	544
DB	422	CCGCTCGTGGATGGAGAAATAAGAACTCTCAAGGGTGGCAAGATGGATGATCGTC	481
QY	545	CAGAGGAACGAAATGATCAGGAGAACTGAAGGCAACCTCTATGCCAGCTGGAAGCAG	604
DB	482	CAGAGGAACGAAATGATCAGGAGAACTGAAGGCAACCTCTATGCCAGCTGGAAGCAG	541
QY	605	AATGGTTGGAAAGAGAGAAATAGCGGCGGCTGTGGTGGTAAACCAATCCCAAGTTAA	664
DB	542	AATGGTTGGAAAGAGAGAAATAGCGGCGGCTGTGGTGGTAAACCAATCCCAAGTTAA	601
QY	665	GAGATGGATCTGAATGAACTAGACGTGCTCCAGGAGGCTCCAGGCAAGTG	724
DB	602	GAGATGGATCTGAATGAACTAGACGTGCTCCAGGAGGCTCCAGGCAAGTG	661
QY	725	CGGCTTCCAGGCTTCCAAAGCGGAGCGAGTCCCTTCTCGGCAATCCCAATCAGGTC	784
DB	662	CGGCTTCCAGGCTTCCAAAGCGGAGCGAGTCCCTTCTCGGCAATCCCAATCAGGTC	721

QY	785	GCACGTGAATCAGATCTCCAGGTAAGGAGAAAGAGTTTCCCAAGTCCCTTTTC	844
DB	722	GCACGTGAATCAGATCTCCAGGTAAGGAGAAAGAGTTTCCCAAGTCCCTTTTC	781
QY	845	AGAGTGCAGAAATCACACACCCCGAGAGCCCTTCCACAGATGGCTTCTCACCATATA	904
DB	782	AGAGTGCAGAAATCACACACCCCGAGAGCCCTTCCACAGATGGCTTCTCACCATATA	841
QY	905	GCCCTGAGGAAACAAACCGCGGTGTTAAACAGTGTGCGGCGCAGACTCTACTCTGC	964
DB	842	GCCCTGAGGAAACAAACCGCGGTGTTAAACAGTGTGCGGCGCAGACTCTACTCTGC	901
QY	965	AGCAGATAGGCGCTTAACCTTCTCTGATTGGAGAGACAGCCCGCAGCAATAAATACCGG	1024
DB	902	AGCAGATAGGCGCTTAACCTTCTCTGATTGGAGAGACAGCCCGCAGCAATAAATACCGG	961
QY	1025	TGTTTATGGGCTTCAGAACTGCACTGCGAGCAATCTCTGTTATCATCTGCTAT	1084
DB	962	TGTTTATGGGCTTCAGAACTGCACTGCGAGCAATCTCTGTTATCATCTGCTAT	1021
QY	1085	TTGTGATGCTCCGGGTGTTTCAACTAGAACCTTCAGACCCCAATGTTATGGAGAAAACTT	1144
DB	1022	TTGTGATGCTCCGGGTGTTTCAACTAGAACCTTCAGACCCCAATGTTATGGAGAAAACTT	1081
QY	1145	TAAAGAAATTTGAGGTTGAGAGTTTGTTCAGAAATATCACAGTAGCGTAGCTCAAGGA	1204
DB	1082	TAAAGAAATTTGAGGTTGAGAGTTTGTTCAGAAATATCACAGTAGCGTAGCTCAAGGA	1141
QY	1205	TCAAAGCTCCATCTCTGTAACACCACTCCAGAGTTTGTTCACGATGTCAAAATCTCTATA	1264
DB	1142	TCAAAGCTCCATCTCTGTAACACCACTCCAGAGTTTGTTCACGATGTCAAAATCTCTATA	1201
QY	1265	CATTGTCAATCATCTAGTACTTCTAGCTGTAGTTCAGAAAAACAGCATAAAGATGAAGG	1324
DB	1202	CATTGTCAATCATCTAGTACTTCTAGCTGTAGTTCAGAAAAACAGCATAAAGATGAAGG	1261
QY	1325	AACAGATGTGCTTATTTGCTTGTGGCATGCTTGTATGAAGAAAGTCTTACAGTGTGTG	1384
DB	1262	AACAGATGTGCTTATTTGCTTGTGGCATGCTTGTATGAAGAAAGTCTTACAGTGTGTG	1321
QY	1385	AAGACGGCTGAGGAAACAAAGCTGCACCACTGCATGTCAATTTGGGCGAAGAGTGTATA	1444
DB	1322	AAGACGGCTGAGGAAACAAAGCTGCACCACTGCATGTCAATTTGGGCGAAGAGTGTATA	1381
QY	1445	GAAGAAATAGAGAACCTTTAATATGTCCTTGTAGATCTAAGTGGAGATCTCATGATT	1504
DB	1382	GAAGAAATAGAGAACCTTTAATATGTCCTTGTAGATCTAAGTGGAGATCTCATGATT	1441
QY	1505	TCTACAGCCACGAGTGTCAAGTCTGTGGATTCCCTTCTTCCCTCAGAGCTGCACAGC	1564
DB	1442	TCTACAGCCACGAGTGTCAAGTCTGTGGATTCCCTTCTTCCCTCAGAGCTGCACAGC	1501
QY	1565	AGCAACCGTACAGCAGCGCTTTGGCTGATCAGAGGAATCAAGAGAGCAATTTTA	1624
DB	1502	AGCAACCGTACAGCAGCGCTTTGGCTGATCAGAGGAATCAAGAGAGCAATTTTA	1561
QY	1625	ACCTTACTCATTTAGAACTCAGCAAAATCCCTCTGCTTACAAAGATTTAGTGCCAT	1684
DB	1562	ACCTTACTCATTTAGAACTCAGCAAAATCCCTCTGCTTACAAAGATTTAGTGCCAT	1621
QY	1685	GGATTGAGTGTGGAAATGAACTGCTGCTGCTTATTTCTAGAACTGGATGTGA	1744
DB	1622	GGATTGAGTGTGGAAATGAACTGCTGCTGCTTATTTCTAGAACTGGATGTGA	1681
QY	1745	GAGAGATGGCCCTCAGGCGCTCTTTCCCATGATGTGAGTGGGCGCCTGTCTTGGCAATG	1804
DB	1682	GAGAGATGGCCCTCAGGCGCTCTTTCCCATGATGTGAGTGGGCGCCTGTCTTGGCAATG	1741
QY	1805	GGGAGAGCACTGGAAATTTCTGGGCGCAGCTGGAAGCAGCCGAGTGGGAGGCCACCA	1864
DB	1742	GGGAGAGCACTGGAAATTTCTGGGCGCAGCTGGAAGCAGCCGAGTGGGAGGCCACCA	1801
QY	1865	GTGGGTCTTCCAGAGCCAGTATCTCAGGAGATGTGGTGGAGGATGCTGTCGACGCTTCTGT	1924

1802	Db		GTGGGCTTTCCGAGACCAAGTATCTCAGGAGATGTGGTGAGGCAATGCTGCGAGCGTTCTGT	1861
1925	Qy		CAATGTCCTGTGCTGACCCCTGCTCTACAAAGTGTAGCTTGCTGCTCTTATAAAACATTGACAG	1984
1862	Db		CAATGTCCTGTGCTGACCCCTGCTCTACAAAGTGTAGCTTGCTGCTCTTATAAAACATTGACAG	1921
1985	Qy		CCATGCTGGTATATATCTCCTTGCCACAGTTTACGCGAAGAAATCAAACTTCAGAGACTTC	2044
1922	Db		CCAATGCTGGTATATATCTCCTTGCCACAGTTTACGCGAAGAAATCAAACTTCAGAGACTTC	1981
2045	Qy		TCCAGCCAGTTGTAGACACCATCCTAGTCAAAATGTGCAGATGCCAATAGCCGACCAAGTC	2104
1982	Db		TCCAGCCAGTTGTAGACACCATCCTAGTCAAAATGTGCAGATGCCAATAGCCGACCAAGTC	2041
2105	Qy		AGCTGTCCATATCAACACTGTTGGAATGTGCAAGGCCAAGCAGAGAGTTGGCAGTTG	2164
2042	Db		AGCTGTCCATATCAACACTGTTGGAATGTGCAAGGCCAAGCAGAGAGTTGGCAGTTG	2101
2165	Qy		GCAGAGAAATACATAAAGCTGGATCCATTGGTATTTGGTGGTGTGATTATGTCTTAAAT	2224
2102	Db		GCAGAGAAATACATAAAGCTGGATCCATTGGTATTTGGTGGTGTGATTATGTCTTAAAT	2161
2225	Qy		GTATTTCTTGGAAACCAAACTGAATCAAACTTGGCAAGAACTTCTTGGCCGCTTGTGC	2284
2162	Db		GTATTTCTTGGAAACCAAACTGAATCAAACTTGGCAAGAACTTCTTGGCCGCTTGTGC	2221
2285	Qy		TTATAGATAGACTGTTGTTGGAAATTTCTGCTGAAATTTTATCCTCATATTTGTCAGTACTG	2344
2222	Db		TTATAGATAGACTGTTGTTGGAAATTTCTGCTGAAATTTTATCCTCATATTTGTCAGTACTG	2281
2345	Qy		ATGTTTTCACAGCTGAGCCTGTTGGAATCAGGTATAGAGCTGCTGCCCTTAACT	2404
2282	Db		ATGTTTTCACAGCTGAGCCTGTTGGAATCAGGTATAGAGCTGCTGCCCTTAACT	2341
2405	Qy		TTGCTTTGCACTCCATTTGATAATTTCCACATCAATGTTGGCAAACTTTCAGAGGATCT	2464
2342	Db		TTGCTTTGCACTCCATTTGATAATTTCCACATCAATGTTGGCAAACTTTCAGAGGATCT	2401
2465	Qy		ACTTGAGTCTGCAAGATGGTTACTACAGTACCCCATGTTTTCAAAACCTTAGAAAA	2524
2402	Db		ACTTGAGTCTGCAAGATGGTTACTACAGTACCCCATGTTTTCAAAACCTTAGAAAA	2461
2525	Qy		TGCTGAGTGTGTTCCAG--TTTCCACTCACTTCCAGGATGCGTCGCGTTTGATGGCTA	2581
2462	Db		TGCTGAGTGTGTTTCCAGTGTGTTTCCACTCACTTCCAGGATGCGTCGCGTTTGATGGCTT	2521
2582	Qy		TTGCAGATGAGTGGAAATTCGCAAGCCATCCAGTTGGCGGTAGAGACACATTTGGATG	2641
2522	Db		ATGCAGATGAGTGGAAATTCGCAAGCCATCCAGTTGGCGGTAGAGACACATTTGGATG	2581
2642	Qy		GTCAACAGGACAGC--TTTCTTGCAAGCATGTGTTCCAAACAACTATCTGGAACCCACAGA	2699
2582	Db		GACAAACACAAACAGCTTTTGCAGGATCTGTTTCCCAACAACTATCTGGAACCCACAGA	2641
2700	Qy		GAAACAGTTTCCCC--TGAGTGCACAGTCCAAATTTAGAGAAAACTGGAAGAGGATTTATGCTA	2758
2642	Db		GAAACAGTTTCCCCCTTGAGTGCACAGTCCAAATTTAGAGAAAACTGGAAGAGGATTTATGCTA	2701
2759	Qy		CAAAATCAGTGCCAGTTTCAGAGACATTTCTGAGAGACTGGCCAGCATTTTCAGTAGGAC	2818
2702	Db		CAAAATCAGTGCCAGTTTCAGAGACATTTCTGAGAGACTGGCCAGGATTTTCAGTAGGAC	2761
2819	Qy		CTTCTAGTTTCAACACAAACAACTTGCATTTAGAGAAAACTGGAAGAGGATTTGTTCAAA	2878
2762	Db		CTTCTAGTTTCAACACAAACAACTTGCATTTAGAGAAAACTGGAAGAGGATTTGTTCAAA	2821
2879	Qy		CAAAAGGACAGCCCAACAGTCAGTGTGTAACCTCTCTCTTTATCTCATCATTTCCCAAT	2938
2822	Db		CAAAAGGACAGCCCAACAGTCAGTGTGTAACCTCTCTCTTTATCTCATCATTTCCCAAT	2881
2939	Qy		TAATGTTTCCAGCTTGTCAACCCCTCTCTCTTCTACCCCATCTGTACACAGCTGGCACTG	2998

QY 4079 CGTATCTCCATGAAAAACAAATCATTCACAGAGATGTCAAAGGTGCCAATTTGCTAATTG 4138  
Db 4022 CGTATCTCCATGAAAAACAAATCATTCACAGAGATGTCAAAGGTGCCAATTTGCTAATTG 4081  
QY 4139 ACAGCACTGGTCAGAGACTAAGAAATTCAGATTTTGGAGCTGCAGCCAGGTGGCATCAA 4198  
Db 4082 ACAGCACTGGTCAGAGACTAAGAAATTCAGATTTTGGAGCTGCAGCCAGGTGGCATCAA 4141  
QY 4199 AAGGAACCTGGTCAGGAGATTTTCAGGACAAATTCAGGACAAATTCAGGACAAATTCAGGAC 4258  
Db 4142 AAGGAACCTGGTCAGGAGATTTTCAGGACAAATTCAGGACAAATTCAGGACAAATTCAGGAC 4201  
QY 4259 CTGAGGTACTAAGAGGTCAACAGATATGAAGGACCTGTGATGTATGAGTGTGGCTGTG 4318  
Db 4202 CTGAGGTACTAAGAGGTCAACAGATATGAAGGACCTGTGATGTATGAGTGTGGCTGTG 4261  
QY 4319 CTATATAGAAATGGCTTGTCGAAACCAACCATGGAATGCAGAAACACCTCCAAATCATC 4378  
Db 4262 CTATATAGAAATGGCTTGTCGAAACCAACCATGGAATGCAGAAACACCTCCAAATCATC 4321  
QY 4379 TTGCTTTGATATTTAAGATTCTAGTGCACACTGCTCCATCGATCCCTTCACATTTGT 4438  
Db 4322 TTGCTTTGATATTTAAGATTCTAGTGCACACTGCTCCATCGATCCCTTCACATTTGT 4381  
QY 4439 CTCCTGGTTTACGAGATGGCTCTTCGTTGTTTGTAGAACTTCAACCTCAGACAGACCTC 4498  
Db 4382 CTCCTGGTTTACGAGATGGCTCTTCGTTGTTTGTAGAACTTCAACCTCAGACAGACCTC 4441  
QY 4499 CATCAAGAGACTACTGAAGCATCCAGTCTTTTCTGCTACTACATGGTAG 4545  
Db 4442 CATCAAGAGACTACTGAAGCATCCAGTCTTTTCTGCTACTACATGGTAG 4488

RESULT 6  
ID AAS66059 standard; cDNA; 4492 BP.  
XX AAS66059;  
AC AAS66059;  
DT 13-FEB-2002 (first entry)  
DE DNA encoding novel human diagnostic protein #1863.  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US008631.  
XX 31-MAR-2000; 2000US-00540217.  
XX 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
XX P-PSDB; ABG01872.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX Claim 1; SEQ ID NO 1863; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have application in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 4492 BP; 1266 A; 1057 C; 1101 G; 1067 T; 0 U; 1 Other;  
Query Watch 83.0%; Score 4354; DB 5; Length 4492;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 4445; Conservative 0; Mismatches 36; Indels 10; Gaps 6;  
QY 65 CGAGCCCTGAGCAGCGCGCGCGAGAGCCCTCAAGCGAGAGCGCGCGCGCGCTG 124  
Db 2 CGAGCCCTGAGCAGCGCGCGCGAGAGCCCTCAAGCGAGAGCGCGCGCGCGCTG 61  
QY 125 CGCGGGACTGCTGGGAGGCGGCGCGCGGCGCGAGCGCGCGGACTGCGCGCGCG 184  
Db 62 CGCGGGACTGCTGGGAGGCGGCGCGGCGCGGCGCGGCGGCGGCGGCGGCGG 121  
QY 185 GGCAGCTGCGCAAGTGGCGAGTGTGGAGCTGGAGCTGGAGCGCGCTTCTTCC 244  
Db 122 GGCAGCTGCGCAAGTGGCGAGTGTGGAGCTGGAGCGCGCTTCTTCC 181  
QY 245 TTGCGCGCTCAGCGCGCGCTCTCTGACTTCCCGCTCCCGCGCGCGCGCGCGCG 304  
Db 182 TTGCGCGCTCAGCGCGCGCTCTCTGACTTCCCGCTCCCGCGCGCGCGCGCGCG 241  
QY 305 GAGTGGGACCGGCTTCCAGCGCTGTGGCGGTGCGCGCGCGCGCGCGCGCGCGCG 364  
Db 242 GAGTGGGACCGGCTTCCAGCGCTGTGGCGGTGCGCGCGCGCGCGCGCGCGCGCG 301  
QY 365 GCGCGCGCGCGCTTACCGAGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 424  
Db 302 GCGCGCGCGCGCTTACCGAGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 361  
QY 425 CGGCGCGCGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 484  
Db 362 CGGCGCGCGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 421  
QY 485 CGGCTCGTGAATGAGAGAAATTAAGAACTCTCAAGGGGTTCACAGATGATGATGTC 544  
Db 422 CGGCTCGTGAATGAGAGAAATTAAGAACTCTCAAGGGGTTCACAGATGATGATGTC 481  
QY 545 CAGAGGAACGAATGATCAGGAGAAATCTGAAGGCACTGTATGCCAGCGCTGGAAGCAGC 604  
Db 482 CAGAGGAACGAATGATCAGGAGAAATCTGAAGGCACTGTATGCCAGCGCTGGAAGCAGC 541  
QY 605 AATGGTTGGAAGAGAGAAATAGCGGAGCGCTGTGTGTGTAAACCAATCCCGATTAAAG 664  
Db 542 AATGGTTGGAAGAGAGAAATAGCGGAGCGCTGTGTGTGTAAACCAATCCCGATTAAAG 601  
QY 665 GAGATGGATCTGAATGAATCACTTACGAGCTGAGTCTCCAGGAGAGGTCCAGCAAGTGT 724  
Db 602 GAGATGGATCTGAATGAATCACTTACGAGCTGAGTCTCCAGGAGAGGTCCAGCAAGTGT 661  
QY 725 CGGCTTCCAGCGCTTCCAAAGCGCGAGCGAGTCTTCTCTGGCAACTCCCGATCAGTTC 784

662 CGGCTTACACAGCTTCCAAAGCCGAGCGAGTCCTCTCTCTGCGCAACTCCCATCAGGTC 721 Db  
785 GCACAGTGAATCAGAACTCTCCAGAGTAAAGAGAAAAGAGTTTCCCGAGTGCCTTTTC 844 Qy  
722 GCACAGTGAATCAGAACTCTCCAGAGTAAAGAGAAAAGAGTTTCCCGAGTGCCTTTTC 781 Db  
845 AGAGTGGCAGAAATCACACACCCCGAAGAGCCCTTCCACAGATGGCTTTCTACCAATATA 904 Qy  
782 AGAGTGGCAGAAATCACACACCCCGAAGAGCCCTTCCACAGATGGCTTTCTACCAATATA 841 Db  
905 GCCCTGAGAAACAAACCGCGTGTAAACAAAGTGAAGCGGCGAGACTGTACTTACTGC 964 Qy  
842 GCCCTGAGAAACAAACCGCGTGTAAACAAAGTGAAGCGGCGAGACTGTACTTACTGC 901 Db  
965 AGCAGATAGGCGCTAACTCTTCTCTGATGGAGGAGACAGCCCAAGAAATACCGGG 1024 Qy  
902 AGCAGATAGGCGCTAACTCTTCTCTGATGGAGGAGACAGCCCAAGAAATACCGGG 961 Db  
1025 TGTATATGGGCGCTCAGAACTGCAGCTGTGACGTGGAACATCTGTATTCTATCTGCTAT 1084 Qy  
962 TGTATATGGGCGCTCAGAACTGCAGCTGTGACATGGAACATCTGTATTCTATCTGCTAT 1021 Db  
1085 TTGTGATGCTCGGGTGTTCCTCAACTAGAACCTTCAGACCCCAATGTTATGGAGAAAAACTT 1144 Qy  
1022 TTGTGATGCTCGGGTGTTCCTCAACTAGAACCTTCAGACCCCAATGTTATGGAGAAAAACTT 1081 Db  
1145 TAAAGAAATTTGAGGTTGAGAGTTTGTTCAGAAATATCAGTAGGCGTAGCTCAGGA 1204 Qy  
1082 TAAAGAAATTTGAGGTTGAGAGTTTGTTCAGAAATATCAGTAGGCGTAGCTCAGGA 1141 Db  
1205 TCAAGAGCTCCATCTCGTAAACACCATCCAGAAAGTTTGTTCACGCAATGTCAAATCTCATA 1264 Qy  
1142 TCAAGAGCTCCATCTCGTAAACACCATCCAGAAAGTTTGTTCACGCAATGTCAAATCTCATA 1201 Db  
1265 CATGTGATCATCTAGTACTTCTAGTCTAGTTCAGAAACAGCATAAAGATCAAGAGG 1324 Qy  
1202 CATGTGATCATCTAGTACTTCTAGTCTAGTTCAGAAACAGCATAAAGATCAAGAGG 1261 Db  
1325 AACAGATGTCTCTATTTGCTGTGGCATGCTTGTATGAAGAAAGTCTTACAGTGTGTG 1384 Qy  
1262 AACAGATGTCTCTATTTGCTGTGGCATGCTTGTATGAAGAAAGTCTTACAGTGTGTG 1321 Db  
1385 AAGAGCGGTGAGGAACAGCTGACACCACTGATGTCAAATTTGGCGAGAGAGTGA 1444 Qy  
1322 AAGAGCGGTGAGGAACAGCTGACACCACTGATGTCAAATTTGGCGAGAGAGTGA 1381 Db  
1445 GAAGAAATAGAAACCTTTAATATGTCCCTTTGTAGATCTAAGTGGAGATCTCATGATT 1504 Qy  
1382 GAAGAAATAGAAACCTTTAATATGTCCCTTTGTAGATCTAAGTGGAGATCTCATGATT 1441 Db  
1505 TCTACAGCCAAGTGTGCAAGTCTGTGGATTCCTTCTTCCCTCAGAGTGCACAGC 1564 Qy  
1442 TCTACAGCCAAGTGTGCAAGTCTGTGGATTCCTTCTTCCCTCAGAGTGCACAGC 1501 Db  
1565 AGCAAAACCTTACAGAGAGCCCTTTGGCTGGATCAGAGGAATCAAGAGAGCAATTTTA 1624 Qy  
1502 AGCAAAACCTTACAGAGAGCCCTTTGGCTGGATCAGAGGAATCAAGAGAGCAATTTTA 1561 Db  
1625 ACCTTACTCATTATGGAATCAGAAATCCCTCTCTGCTTACAAAGATTTAGCTAGCCAT 1684 Qy  
1562 ACCTTACTCATTATGGAATCAGAAATCCCTCTCTGCTTACAAAGATTTAGCTAGCCAT 1621 Db  
1685 GGNATTCAGGTTTGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1744 Qy  
1622 GGNATTCAGGTTTGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1681 Db  
1745 GAGAGATGGCCCTCAGGCGTCTTTTCCCATGATGTACAGTGGGCGCCCTGCTGTGGCAATG 1804 Qy  
1682 GAGAGATGGCCCTCAGGCGTCTTTTCCCATGATGTACAGTGGGCGCCCTGCTGTGGCAATG 1741 Db  
1805 GGSAGAGCACTGAATTTCTGGGGCAGCAGTGGAGCAGCCGAGTGGGGAGCCACCA 1864 Qy  
1742 GGSAGAGCACTGAATTTCTGGGGCAGCAGTGGAGCAGCCGAGTGGGGAGCCACCA 1801 Db

1865 GTGGGTCTTCCAGACCAGTATCTCAGGAGATGTGGTGGAGGCATGTCTGCAGCGTCTGT 1924 Qy  
1802 GTGGGTCTTCCAGACCAGTATCTCAGGAGATGTGGTGGAGGCATGTCTGCAGCGTCTGT 1861 Db  
1925 CAATGGTCTGTGCTGACCCCTGTCTACAAAGTGTAGTGTCTTAAACATTTGAGAG 1984 Qy  
1862 CAATGGTCTGTGCTGACCCCTGTCTACAAAGTGTAGTGTCTTAAACATTTGAGAG 1921 Db  
1985 CCATGTGTATATATCTCTCTTCCACAGCTTTAGCGGAAAGAAATCAAACTTCAGAGACTTC 2044 Qy  
1922 CCATGTGTATATATCTCTCTTCCACAGCTTTAGCGGAAAGAAATCAAACTTCAGAGACTTC 1981 Db  
2045 TCCAGCCAGTTGTAGACACCACTCTAGTCAAAATGTGCAAGATGCCAATAGCCGCAAGTTC 2104 Qy  
1982 TCCAGCCAGTTGTAGACACCACTCTAGTCAAAATGTGCAAGATGCCAATAGCCGCAAGTTC 2041 Db  
2105 AGCTGTCCATATCAACACTGTTTGGAACTGTGCAAAAGGCCAAAGCAGAGAGTTGGCAGTTG 2164 Qy  
2042 AGCTGTCCATATCAACACTGTTTGGAACTGTGCAAAAGGCCAAAGCAGAGAGTTGGCAGTTG 2101 Db  
2165 GCAGAGAAATATCAAAAGCTGGATCCATTTGGTGTATTTGGTGTGATTTATGCTTTAAAT 2224 Qy  
2102 GCAGAGAAATATCAAAAGCTGGATCCATTTGGTGTATTTGGTGTGATTTATGCTTTAAAT 2161 Db  
2225 GTATTTCTTGGAAACCAAACTGAATCAAACTGAATTTGGCAAGAACTTCTTGGCCGCTTTGTC 2284 Qy  
2162 GTATTTCTTGGAAACCAAACTGAATCAAACTGAATTTGGCAAGAACTTCTTGGCCGCTTTGTC 2221 Db  
2285 TTATAGATAGACTGTTTGGAAATTTCTGCTGAAATTTATCTCTCATATTTGTCAGTACTG 2344 Qy  
2222 TTATAGATAGACTGTTTGGAAATTTCTGCTGAAATTTATCTCTCATATTTGTCAGTACTG 2281 Db  
2345 ATGTTTCAAGCTGAGCCCTGTTGAAATCAGGTATATAAGAGCTGTCTCTCTTTAACT 2404 Qy  
2282 ATGTTTCAAGCTGAGCCCTGTTGAAATCAGGTATATAAGAGCTGTCTCTCTTTAACT 2341 Db  
2405 TTGCTTTGAGTCCATTTGATTAATTTCCACTCAATGGTGGCAAACTTTCCAGAGAGTCT 2464 Qy  
2342 TTGCTTTGAGTCCATTTGATTAATTTCCACTCAATGGTGGCAAACTTTCCAGAGAGTCT 2401 Db  
2465 ACTTTGAGTTCTGCAAGAAATGTTTACTACAGTACCCCATGTTTTCAAAACCTTTAGAAA 2524 Qy  
2402 ACTTTGAGTTCTGCAAGAAATGTTTACTACAGTACCCCATGTTTTCAAAACCTTTAGAAA 2461 Db  
2525 TGTGAGTGTTCAG ---TTCCACTCTTACAGAGGATGCTGTCCGCTTTGATGGCTA 2581 Qy  
2462 TGTGAGTGTTCAGTGTTCCTCACTTCCAGGATGCTGTCCGCTTTGATGGCTT 2521 Db  
2582 TTGAGATGAGTGGGAAATTTCCGAGCCATCCAGTTGGGCGTAGAAGACACTTTTGGATG 2641 Qy  
2522 ATGAGATGAGTGGGAAATTTCCGAGCCATCCAGTTGGGCGTAGAAGACACTTTTACAAC 2581 Db  
2642 GTCAACAGGACAGC ---TTCTTGGAGGCATCTGTTCCCAACACTATCTGGAACCCACAGA 2699 Qy  
2582 GACAAACAAACACAGCTTTTGCAGGCATCTGTTCCCAACACTATCTGGAACCCACAGA 2641 Db  
2700 GAACAGTTCCTCC ---TGAGTGCACAGTCCATTTAGAGAAAACCTGGAAGAGTATGTGCTA 2758 Qy  
2642 GAACAGTTCCTCCCTTGAGTGCACAGTCCATTTAGAGAAAACCTGGAAGAGTATGTGCTA 2701 Db  
2759 CAAAAATTTGAGTGGCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGCATTTCTAGTAGGAC 2818 Qy  
2702 CAAAAATTTGAGTGGCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGGATTTCTAGTAGGAC 2761 Db  
2819 CTCTAGTTTCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2878 Qy  
2762 CTCTAGTTTCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2821 Db  
2879 CAAAAGCAGACCCCAACAGTGTGTAACCTCTCTCTTTATCTCATTCATTCATTCATTCAT 2938 Qy  
2822 CAAAAGCAGACCCCAACAGTGTGTAACCTCTCTCTTTATCTCATTCATTCATTCATTCAT 2881 Db

QY 2939 TAATGTTTCCAGCCTTGTCAACCCCTTCTTCTTACCCCATCTGTACCAGCTGGCACTG 2998  
Db 2882 TAATGTTTCCAGCCTTGTCAACCCCTTCTTCTTACCCCATCTGTACCAGCTGGCACTG 2941  
QY 2999 CAACAGATGTCCTTAAGCATAGACTTCAGGATTCATTCCTGAGAAATACCTTCTGCAT 3058  
Db 2942 CAACAGATGTCCTTAAGCATAGACTTCAGGATTCATTCCTGAGAAATACCTTCTGCAT 3001  
QY 3059 CTCCTCAAAACACAGCGCAAGTTTCTCTTACCAATTCACAGAAACTGTCCTGAAACAAAG 3118  
Db 3002 CTCCTCAAAACACAGCGCAAGTTTCTCTTCAATTCACAGAAATGTCCTGAAACAAAG 3061  
QY 3119 ACTCAGATAAATTTCCCCAGTCTTTTACTCAGTCAAGACCTTGCCTTCCAGTAAATAC 3178  
Db 3062 ACTCAGATAAATTTCCCCAGTCTTTTACTCAGTCAAGACCTTGCCTTCCAGTAAATAC 3121  
QY 3179 ACAGGCCAAAGCCATCTAGACCTACCCAGGTATACAAAGTAACACAGGAGATCCCTCAA 3238  
Db 3122 ACAGGCCAAAGCCATCTAGACCTACCCAGGTATACAAAGTAACACAGGAGATCCCTCAA 3181  
QY 3239 AAAATAGCATGACATTTGATCTGAACAGTAGTTCCAAATGTGATGACAGCTTTGGCTGTA 3298  
Db 3182 AAAATAGCATGACATTTGATCTGAACAGTAGTTCCAAATGTGATGACAGCTTTGGCTGTA 3241  
QY 3299 GCAGCAATAGTAGTAATGCTGTATACCCAGTGCAGACAGTGTTCACCCAGCTAGAGG 3358  
Db 3242 GCAGCAATAGTAGTAATGCTGTATACCCAGTGCAGACAGTGTTCACCCAGCTAGAGG 3301  
QY 3359 AGAAATGCAGATTAGATGTCAATACAGAGCTCAACTCCAGTATTGAGGACCTTCTTGAAG 3418  
Db 3302 AGAAATGCAGATTAGATGTCAATACAGAGCTCAACTCCAGTATTGAGGACCTTCTTGAAG 3361  
QY 3419 CATCTATGCCCTTCAAGTATACAAAGTAACTTTTAAAGTCAAGAGTTCCTGCTGCTC 3478  
Db 3362 CATCTATGCCCTTCAAGTATACAAAGTAACTTTTAAAGTCAAGAGTTCCTGCTGCTC 3421  
QY 3479 CTGAAAGGCTGAAATGATGATACCTCAAGATGATGTGAATCATTAATCAAAAGTGCA 3538  
Db 3422 CTGAAAGGCTGAAATGATGATACCTCAAGATGATGTGAATCATTAATCAAAAGTGCA 3481  
QY 3539 AAGAGAAGATGAAAGCTGAAGAAAGAGCTTTAGCAATTTGCCATGGCAATGTGACGGT 3598  
Db 3482 AAGAGAAGATGAAAGCTGAAGAAAGAGAGCTTTAGCAATTTGCCATGGCAATGTGACGGT 3541  
QY 3599 CTCAGGATGCCCTCCCATAGTTCTCAGTGCAGGTTGAAATGGAGAAGATATCATCA 3658  
Db 3542 CTCAGGATGCCCTCCCATAGTTCTCAGTGCAGGTTGAAATGGAGAAGATATCATCA 3601  
QY 3659 TTATTCAACAGGATACACAGAGACTCTACAGGACATACCAAGCAAAACAAACCGTATA 3718  
Db 3602 TTATTCAACAGGATACACAGAGACTCTACAGGACATACCAAGCAAAACAAACCGTATA 3661  
QY 3719 GAGAGACACTCAATGGCTGAAGGTCAACAGATAGGCTTGGAGCATTTTCTTCTGTT 3778  
Db 3662 GAGAGACACTCAATGGCTGAAGGTCAACAGATAGGCTTGGAGCATTTTCTTCTGTT 3721  
QY 3779 ATCAGGCTCAAGATGTGGAACTGGAACCTTTAATGGCTGTTAAACAGGTGACTTATGTC 3838  
Db 3722 ATCAGGCTCAAGATGTGGAACTGGAACCTTTAATGGCTGTTAAACAGGTGACTTATGTC 3781  
QY 3839 GAAACACATCTTCTGAGCAAGAGAGTAGTAGAGACTTAAGAGAGAGATAGATGCA 3898  
Db 3782 GAAACACATCTTCTGAGCAAGAGAGTAGTAGAGACTTAAGAGAGAGATAGATGCA 3841  
QY 3899 TGAGGCATCTGAATCATCAAAACATCAATAGGATGTTGGAGCCACGTTGAGAGAGCA 3958  
Db 3842 TGAGGCATCTGAATCATCAAAACATCAATAGGATGTTGGAGCCACGTTGAGAGAGCA 3901  
QY 3959 ATTACAACTCTTCAATGGAATGGATGGCAGGGGATCGGTGGCTCATTTGCTGAGTAAAT 4018  
Db 3902 ATTACAACTCTTCAATGGAATGGATGGCAGGGGATCGGTGGCTCATTTGCTGAGTAAAT 3961  
QY 4019 ATGGAGCCTTCAAGAAATCAGTAGTTATTAACTACACTGAACAGTACTCCGTCGCTTT 4078

Db 3962 ATGGAGCCTTCAAGAAATCAGTAGTTATTAACTACACTGAACAGTACTCCGTGGACTTT 4021  
QY 4079 CGTATCTCATGAAACCAAATCATTCACAGAGATGTCAAAGTGCCAAATTTGCTAAATG 4138  
Db 4022 CGTATCTCATGAAACCAAATCATTCACAGAGATGTCAAAGTGCCAAATTTGCTAAATG 4081  
QY 4139 ACAGCACTGGTCAGAGACTTAAGAAATTTGGAGCTGCAGCCAGGTTGGCATCAA 4198  
Db 4082 ACAGCACTGGTCAGAGACTTAAGAAATTTGGAGCTGCAGCCAGGTTGGCATCAA 4141  
QY 4199 AAGGAATCTGGTCAGAGAGAGTTTCAGGGAACAATTTCTGGGGAACAATTTGCAATTTATGGCAC 4258  
Db 4142 AAGGAATCTGGTCAGAGAGAGTTTCAGGGAACAATTTCTGGGGAACAATTTGCAATTTATGGCAC 4201  
QY 4259 CTGAGGTACTTAAGAGGTCAACAGTATGGAAGAGAGCTGTGATGTATGGAGTGTGGCTGTG 4318  
Db 4202 CTGAGGTACTTAAGAGGTCAACAGTATGGAAGAGAGCTGTGATGTATGGAGTGTGGCTGTG 4261  
QY 4319 CTATTATAGAAATGGCTTGTGCAAAACCAACCACTGGAATGCAGAAACAACTCCAATCATC 4378  
Db 4262 CTATTATAGAAATGGCTTGTGCAAAACCAACCACTGGAATGCAGAAACAACTCCAATCATC 4321  
QY 4379 TTGCTTTGATATTTAAGATTGCTAGTGAACCTGCTCCATCGATCCCTTCACATTTGT 4438  
Db 4322 TTGCTTTGATATTTAAGATTGCTAGTGAACCTGCTCCATCGATCCCTTCACATTTGT 4381  
QY 4439 CTCCTGTTTACG-AGATGTGCTCTTCTGTTGTT-AGAACTTCAACCT--CAGGACAGA 4494  
Db 4382 CTCCTGTTTACGAAAGATGTGCTCTTCTGTTGTTTAAAGAACTTCAACCTTCANGGACAGA 4441  
QY 4495 CTTCCATCAAGAGAGCTACTGAGGATCCAGTCTTTTCGTACTACATGGTAG 4545  
Db 4442 CTTCCATCAAGAGAGCTACTGAGGATCCAGTCTTTTCGTACTACATGGTAG 4492

## RESULT 7

ABT42340

ID ABT42340 standard; DNA; 5180 BP.

XX AC ABT42340;

XX DT 26-JUN-2003 (first entry)

XX XX Toxicity modelling related rat gene SEQ ID No 2042.

XX XX Toxic effect; gene expression profile; renal toxicity; toxicity marker;  
XX XX database; drug screening; toxicity assay; rat; ds.

XX OS Rattus norvegicus.

XX PN W0200295000-A2.

XX XX 28-NOV-2002.

XX XX 22-MAY-2002; 2002W0-US016173.

XX XX 22-MAY-2001; 2001US-0292335P.

XX XX 13-JUN-2001; 2001US-0297523P.

XX XX 19-JUN-2001; 2001US-0298925P.

XX XX 10-JUL-2001; 2001US-0303807P.

XX XX 10-JUL-2001; 2001US-0303808P.

XX XX 28-AUG-2001; 2001US-0303810P.

XX XX 27-SEP-2001; 2001US-0324928P.

XX XX 22-OCT-2001; 2001US-0330462P.

XX XX 01-NOV-2001; 2001US-0330867P.

XX XX 21-NOV-2001; 2001US-0331805P.

XX XX 06-DEC-2001; 2001US-0336144P.

XX XX 19-DEC-2001; 2001US-0340873P.

XX XX 21-FEB-2002; 2002US-0357842P.

XX XX 21-FEB-2002; 2002US-0357843P.

XX XX 21-FEB-2002; 2002US-0357844P.

PR 15-MAR-2002; 2002US-0364134P.  
PR 08-APR-2002; 2002US-0370144P.  
PR 08-APR-2002; 2002US-0370206P.  
PR 08-APR-2002; 2002US-0370247P.  
PR 17-APR-2002; 2002US-0372794P.  
PR 21-APR-2002; 2002US-0371679P.  
XX (GENE-) GENE LOGIC INC.  
PA  
XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;  
XX WPI; 2003-148464/14.  
XX  
XX Predicting at least one toxic effect of a compound, useful for toxicity  
PT modeling, comprises preparing a gene expression profile of a tissue or  
PT cell sample exposed to the compound, and comparing the gene expression  
PT profile to a database.  
XX  
XX Example 4; Page; 446pp; English.  
PS  
XX The invention relates to a novel method of predicting at least one toxic  
CC effect of a compound. The method comprises a gene expression profile of a  
CC tissue or cell sample exposed to the compound, and comparing the gene  
CC expression profile to a database comprising at least part of the data or  
CC information given in the specification. The methods are useful for  
CC predicting at least one toxic effect of a compound, predicting the  
CC progression of a toxic effect of a compound, predicting the renal  
CC toxicity of a compound, or identifying toxicity markers in tissues or  
CC cells exposed to known renal toxin. The genes are useful as toxicity  
CC markers in drug screening and toxicity assays, in monitoring disease or  
CC physiological states, or disease progression. This polynucleotide  
CC represents a rat DNA sequence relating to the toxic effect database  
CC described in the specification. NOTE: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from the World Intellectual Property  
CC Organization  
XX  
XX Sequence 5180 BP; 1225 A; 1521 C; 1443 G; 991 T; 0 U; 0 Other;  
Query Match 65.2%; Score 3420.8; DB 7; Length 5180;  
Best Local Similarity 84.5%; Pred. No. 0;  
Matches 4020; Conservative 0; Mismatches 647; Indels 91; Gaps 12;  
QY 1 GAGAAATGCGCGCGCGGGGATCGCGCTCGTGTGGGATTCGCGGCGCCAGG 60  
DB 510 GAGAAATGCGCGCGCGCGCGGATCGCGCTCGTGTGGGATTCGCGGCGCCAGG 569  
QY 61 GCTACGAGCCCTGAGCAGCGCGCGCGGAGAGCCCTCAAGCGAGCAGCGCGCGCG 120  
DB 570 GCGCGAGCCCGAGCGCGCGCGCGCGCGCGAGCTCTCCAGGAAAGCGCGCGCGCA 629  
QY 121 GCTGCCGCGGACTGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
DB 630 GCGCGCGCGGCGCTGCTGCGGAGACTGGCAGCGCGCGCGCGCGCGCGCGCG 689  
QY 181 CGCGCGCAGCTGCGCAAGTGGCGGAGTGTGGAGCTGGACAGCTGCGTGGAGCGCGCTC 240  
DB 690 CGCGCAGCTGCGCAAGTAAAGAGTGTGGAGCTGGACAGCTGCGCGAGCAGCGCTC 749  
QY 241 TTCTTTCGCGCTCAGCGCGCGCTCTCGACTTCCCGTCCCGGAGCGCGCGCGCGCA 300  
DB 750 TTCTTTCGCGCTCAGCGCGCGCTCTCGACTTCCCGTCCCGGAGCGCGCGCGCG 809  
QY 301 CGCGGAGTGGGACCGCGCTTCCAGCGCTGTGGCGGCTGCGCGCGCGCGCGCGCG 360  
DB 810 GCTGCGAGGCGAGTGGCTTCCAGCTGCGCGCGGAGCGCGCGCGCGCGCGAGT 869  
QY 361 CG 420  
DB 870 CGTGGCGGCTCCCACTCTCGAGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 929  
QY 421 GCAGCG 480

930 GCGGG-----GCCGAGCCGCGCTCTGCGCGGCC 959  
481 CCGCGCGCTGTCGAGATGAGAAATCTCAAGGGTTCACAAAGATGATGAT 540  
960 CCGCTCCGTCGAGAGATGAGAAATCTCAAGGGTTCACAAAGATGATGAT 1019  
541 CGTCCAGAGAACGANTGATCAGGAGAACTGAGGCAACCTGATGATGATGAT 600  
1020 CGCCAGAGAGCGAATGATCAGGAGAACTGAGGCAACCTGATGATGATGAT 1079  
601 CAGCAATGTTGAAAGAGGAAATAGCGAGGCGCTGTGTTGTTGTTGTTGTT 660  
1080 CACGAGTGTGTAAGAGGAGGAAACAGAGAGGCGCTGTGTTGTTGTTGTTG 1139  
661 AAGAGAGATGATCTCAAAATGATCATTAGCAGTGTGTTGTTGTTGTTGTTG 720  
1140 AAGAGAGATGATCTCAAAATGATCATTAGCAGTGTGTTGTTGTTGTTGTTG 1199  
721 AGTGGCGCTTCCAGAGTTCGAAAGCGAGCGCTTCTCTCTGCGCAATCCCCATCA 780  
1200 GGTCTGCTGCCACCGCTCCCAAGGCGCGAGCGCGCTCTCTGGAAGCTCCCCATCA 1259  
781 GGTCCGACAGTGAATCAGAAATCTCAGAGTGAAGAGAAAGAGTTTCCGAGTGCCT 840  
1260 GCGCGCTCAGGAGGAGCGCGCGCTGTGTAACAAAGTGTGAGGCGCGCTTCC 1319  
841 TTTCCAGAGTGGCAGAAATCACACCGCGAGGCGCTTCCAGAGTGGCTTCTCACCA 900  
1320 TTTCCAGAGTGGCAGAAATCACACCGCGAGGCGCTTCCAGAGTGGCTTCTCACCG 1379  
901 TATAGCCCTGAGGAAACAAACCGCGCTGTGTAACAAAGTGTGAGGCGCGAGCTGACTTA 960  
1380 TACAGCCGAGAGAGAGCGCGCGCTGTGTAACAAAGTGTGAGGCGCGAGTGTACCTC 1439  
961 CTCAGCAGATAGCGGCTTAATCTTTCTGATTTGGAGGAGAGCAGCCGAGCAATAATAC 1020  
1440 CTCAGCAGATAGCGGCTTAATCTTTCTGATTTGGAGGAGAGCAGTCCAGCAATAATAC 1499  
1021 CGCGTGTATTGCGGCTCAGAACTCAGCTGTCAGCTGAGTGAACATCTGTATTCTG 1080  
1500 CGCGTGTATTGCGGCTCAGAACTCAGCTGTCAGCTGAGTGAACATCTGTATTCTG 1559  
1081 CTATTTGTGATGCTCGGGTGTGTTAACTAGAACCTTCAGAGCCCAATGTTATGAGAAA 1140  
1560 TTGTTGTGATGCTCGGGTGTGTTAACTAGAACCTTCAGAGCCCAATGTTATGAGAAA 1619  
1141 ACTTTAAGAAATTTGAGTTGAGTGTGTTTCCAGAAATATCAGAGTGGCGTAGCTCA 1200  
1620 ACTTTAAGAAATTTGAGTTGAGTGTGTTTCCAGAAATATCAGAGTGGCGTAGCTCA 1679  
1201 AGGATCAAGCTCCATCTCGTACACCATCCAGAGTGTGTTTCCAGCAATGTCATATCT 1260  
1680 AGAATCAAGCTCCATCTCGTACACCATCCAGAGTGTGTTTCCAGCAATGTCATATCT 1739  
1261 CATACATGTCATCATCTAGTACTTCTAGCTGTAGTTCCAGAAACAGCAATAAGGATGA 1320  
1740 CACACATGTCATCGTCTAGCAGCATCCATCTAGTTCCAGAAACAGCAATAAGGATGA 1799  
1321 GAGGACAGATGTCCTATTTGCTGTTGGCGATCTGTGATGAGAAAGTCTTACAGTG 1380  
1800 GAGGACAGATGTCCTATTTGCTGTTGGCGATCTGTGATGAGAAAGTCTTACAGTG 1859  
1381 TGTGAAGACGCGTGCAGGAAACAGCTGCACCACTGCATGTCAATTTTGGGCGAGAG 1440  
1860 TGTGAAGACGCGTGCAGGAAACAGCTGCACCACTGCATGTCAATTTTGGGCGAGAG 1919  
1441 TGTGAAGAAATAGAGAACTTTAATATCTGCTGCTTGTAGATCTAAGTGGAGATCTCAT 1500  
1920 TGTGAAGAAATAGAGAACTTTAATATCTGCTGCTTGTAGATCTAAGTGGAGATCTCAT 1979  
1501 GATTTCTACAGCAGGATGTCAAGTCTGTGGAATTTCCCTTCTTCTTCTTCTCAGAGTGA 1560  
1980 GACTTCTACAGCAGGATGTCAAGTCTGTGGAATTTCCCTTCTTCTTCTTCTCAGAGTGA 2039







Db 4170 AGAAGACACCGAGTGGCTGAAGGGGCGAGAGATAGCCCTCGAGCATTTCTTCTGT 4229  
Qy 3778 TATCAGGCTCAAGATGTGGAACTTGAATTAATGCTGTAAACAGGTGACTTATGTC 3837  
Db 4230 TACCAAGCACAGGATGTGGCACTTGAATTAATGCTGTAAACAGGTGACTTATGTC 4289  
Qy 3838 AGAAGACATCTTCTGAGCAGAGAGATAGTAGAGACTTAAGAGAGATAGATG 3897  
Db 4290 AGAAGACATCTTCTGAGCAGAGAGATAGTAGAGACTTGAAGAGATAGATG 4349  
Qy 3898 ATGAGCCATCTGAATCACTCCAAACATCAATAGGATGTTGGAGCCAGCTGTGAGAGAGC 3957  
Db 4350 ATGAGCCATCTCAACCATCCGAAATCATCAAGATGCTGGGGCCAGCTGCGAGAGAGC 4409  
Qy 3958 AATTACATCTCTTCAATTAATGAATGATGCGAGGGGATCGGTGGCTCATTTGCTGAGTAAA 4017  
Db 4410 AACTACATCTCTTCAATTAATGAATGATGCGAGGGGATCGGTGGCTCATTTGAGTAAA 4469  
Qy 4018 TATGAGCCTTCAAGATCACTAGTATTATTAACCTACATCACTGAACAGTTACTCCGTGGCCTT 4077  
Db 4470 TATGAGCCTTCAAGATCACTAGTATTATTAACCTACATCACTGAACAGTTACTCCGTGGCCTT 4529  
Qy 4078 TCGTATCTCCATGAAACCAATCATTCACAGAGATGTAAGGTGCCAATTTGCTAATT 4137  
Db 4530 TCCTATCTCCACGAGAACCATCATTCACAGAGAGCTCAAGGGGCCAATCTGCTCAT 4589  
Qy 4138 GACAGCACTGTCAGAGACTAAGATTCAGATTTGGAGCTGAGCCAGCTGGCATCA 4197  
Db 4590 GACAGCACCGTCAAGCTGAGATTCAGATTTGGAGCTGAGCCAGCTGGCATCC 4649  
Qy 4198 AAAGAACTGTGAGGAGAGTTTCAAGGACAATTAAGGACAATTAAGGACAATTAAGGACA 4257  
Db 4650 AAAGAACTGTGAGGAGAGTTTCAAGGACAATTAAGGACAATTAAGGACAATTAAGGACA 4709  
Qy 4258 CCTGAGTACTAAGAGTCAACATGATGAGAGGAGCTGATGATGAGTGTGGCTGT 4317  
Db 4710 CCTGAGTACTAAGAGTCAACATGATGAGAGGAGCTGATGATGAGTGTGGCTGT 4769  
Qy 4318 GCTATTATAGAAATGGCTGTGCAAAACACCATCGAATGAGAGAAACACATCCAAATCAT 4377  
Db 4770 GCAATTAAGAAATGGCTGTGCAAAACACCATCGAATGAGAGAAACACATCCAAATCAT 4829  
Qy 4378 CTGCTTTGATATTAAAGTGTAGTCACTACTGCTCACTGATGATGATGATGATGATGATG 4437  
Db 4830 CTGCTTTGATATTAAAGTGTAGTCACTACTGCTCACTGATGATGATGATGATGATGATG 4889  
Qy 4438 TCTCTGCTTTACGAGATGTGGCTCTTCTGTTTGTAGAACTTCAACCTCAGGACAGACCT 4497  
Db 4890 TCCCGGGCTCGAGAGCTGGCTCTGGCTGTTTGTAGAACTTCAACCTCAGGACAGACCT 4949  
Qy 4498 CCATCAAGAGAGCTACTGAAGATCCAGTCTTTGTACTAGATGATGATGATGATGATGATG 4557  
Db 4950 CCGTCAAGAGAGCTACTGAAGATCCAGTCTTTGTACTAGATGATGATGATGATGATGATG 5003  
Qy 4558 ATCAACTACAGTAGAAGACAGAGTGTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4617  
Db 5004 -----GCTCAGGCTGCGAACAAG-AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5048  
Qy 4618 TGATATTTACATGAGGAGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4677  
Db 5049 TGATATGCTGTGGCC-TCATACCACTGACCCAG-----AAGAGAGAGAGAGAGAGAGAG 5103  
Qy 4678 TACCTAAGTATGATGATGAG 4737  
Db 5104 CACCTAAGATGATGATGAG 5162  
Qy 4738 -AACTAGTGCAGAACTG 4754  
Db 5163 CAACCTGTCAGGAGCTG 5180

RESULT 8

ADB58821  
ID ADB58821 standard; DNA; 5180 BP.  
XX  
AC ADB58821;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Toxicity-related gene, SEQ ID 3847.  
XX  
KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;  
KW drug screening; toxicity assay; ds.  
OS Unidentified.  
XX  
PN WO2003064624-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 31-JAN-2003; 2003WO-US003194.  
XX  
PR 31-JAN-2002; 2002US-00060087.  
PR 15-MAR-2002; 2002US-0364045P.  
PR 15-MAR-2002; 2002US-0364055P.  
PR 30-DEC-2002; 2002US-0436643P.  
XX  
PA (GENE-) GENE LOGIC INC.  
XX  
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;  
XX WPI; 2003-689530/65.  
XX  
PT Predicting a toxic effect of a compound, useful in identifying toxicity  
PT markers in liver tissues or cells for drug screening and toxicity assays,  
PT comprises preparing gene expression profile of tissue or cells exposed to  
PT the compound.  
XX  
PS Claim 1; SEQ ID NO 3847; 1156pp; English.  
XX  
CC The present invention relates to a method for predicting a toxic effect  
CC of a compound. The method comprises preparing a gene expression profile  
CC of a tissue or cell sample exposed to the compound, and comparing the  
CC gene expression profile to a database comprising SEQ ID 1-4925, where  
CC differential expression of the gene indicates at least one toxic effect.  
CC The method is useful for predicting at least one toxic effect of a  
CC compound, predicting hepatotoxicity or the progression of a toxic effect  
CC of a compound, identifying an agent that modulates the onset or  
CC progression of a toxic response, predicting the cellular pathways that a  
CC compound modulates in a cell, and identifying an agent that modulates at  
CC least one activity of a protein. The method and compositions of the  
CC present invention using a database of genes having liver toxin-induced  
CC differential expression are useful in identifying toxicity markers in  
CC liver tissues or cells for drug screening and toxicity assays. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
SQ Sequence 5180 BP; 1225 A; 1521 C; 1443 G; 991 T; 0 U; 0 Other;

Query Match 65.2%; Score 3420.8; DB 9; Length 5180;  
Best Local Similarity 84.5%; Pred. No. 0;  
Matches 4020; Conservative 0; Mismatches 647; Indels 91; Gaps 12;  
Qy 1 GAGAAATGGCG 60  
Db 510 GAGAAATGGCG 569  
Qy 61 GCTACAGAGCTTGGAGCAGCG 120  
Db 570 GCGGCGAGCG 629  
Qy 121 GCTGCCCGCGGAGCTGCTGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
Db 630 GCGGCGCGGAGCTGCTGCGGAGGAGCTGCGGAGGAGCTGCGGAGGAGCTGCGGAGGAG 689

QY 181 CGCGGAGCTGCGCAAAAGTSCGGAGTGTGAGCTGGAACAGCTGCTGAGCAGCCGCTC 240  
DB |||||  
QY 690 CGGAGCAGCTGCGCAAAAGTAAAGAGTGTGAGCTGGAACAGCTGCGGAGCAGCCGCTC 749  
DB |||||  
QY 241 TTCCCTGCGGCTCACCGCCGCTCCTCGACTTCCTCCGCTCGCGGAGCCCGGAGCGCA 300  
DB |||||  
QY 750 TTCCCTCAGCGCTCGCGCCCTGCCCTACTACTTCCCGCTCGCGGAGCCCGGAGCGG 809  
DB |||||  
QY 301 CGGGGAGTGGAGCGGCTTCCAGCTGTGCGGTGCGCGCCGCCGCCACGAGCGCGAGC 360  
DB |||||  
QY 810 GCTGAGGAGGAGTGGCTTCCAGCTGCGCGCGGAGCGCGCACCCCGCGGAGCAGCGAGT 869  
DB |||||  
QY 361 CGCGCGCGCCACCTTACCGAGTCGCTGCGCGCGCGGAGCGCGAGCGCGCTCGAGTCCC 420  
DB |||||  
QY 870 CGCTGCGGCTCCACTCTGCGAGCTGCGCGCGCGGAGCGCGAGCGCGCGCGCGCGCC 929  
DB |||||  
QY 421 GCAGCGCGCGAGCCCGGAGGAGCGCGCGCGCGCGCGCGCGCTCTCTGCGAGCGGCC 480  
DB |||||  
QY 930 GCGGG-----GCCGAGCGCGCTCTGCGAGCGGCC 959  
DB |||||  
QY 481 CCCGCGGCTGATGAGATGGAATAAAGAACTCTCAAGAGGTTGCAACAGATGGATGAT 540  
DB |||||  
QY 960 CCTCGGTCAGAGATGAGATAAAGAACTCTCAAGAGTTGCAACAGATGGATGATGAT 1019  
DB |||||  
QY 541 CTTCCAGAGGAAAGATGATCAGGAGAACTGAAGGCAACTGTATGCGGAGCGCTGGAAG 600  
DB |||||  
QY 1020 GCGCCAGAGGAGCGAATGATCAGGAGAACTCAAGCGGACCTGTATGCGCTGCGTGAAG 1079  
DB |||||  
QY 601 CACGAATGTTTGAAGAGGAAATAGCGAGGCGCTGCTGTTAAACCAATCCAGTT 660  
DB |||||  
QY 1080 CACGAGTGGTTAGAAAGAGAGAAACAGGAGAGCGCTGCTGTTGTTGAACCAATCCCTATT 1139  
DB |||||  
QY 661 AAAGAGATGATCTGAATGAATCACTTAGCAGCTGAGTCTCCAGGAGAGGTCAGGCA 720  
DB |||||  
QY 1140 AAAGAGATGATCTGAATGATTAATTTGACGCTGAGTCTCAAGGAGGCGCAGGCA 1199  
DB |||||  
QY 721 AGTGGGCTTCCAGCTTCCAAAGCCGAGCGAGTCTCTCTGCGCAACTCCCATCA 780  
DB |||||  
QY 1200 GCGCTGTGTGACCAAGCTCCCAAGGGCGGACGAGCGCGCTCTCTGGAAGCTCCCATCA 1259  
DB |||||  
QY 781 GGTCCACAGTGAATCAGAACTCTCCAGAGTAAAGAGAAAGAGTTTCCCGAGTGCCT 840  
DB |||||  
QY 1260 GGGCGCTCAGGAGCGGAACTCCCGAGTGTGAGCGGAAACGAGTGTCCCGAGTGCCT 1319  
DB |||||  
QY 841 TTTGAGTGGAGAAATCACACCCCGGAGAGCGCTTCCAGAGTGGTTCTCACCA 900  
DB |||||  
QY 1320 TTCCAGAGTGGCAGAAATCACACCCAGCTCGAAGAGCGCGCTGCGCAGATGGCTTCTCACCG 1379  
DB |||||  
QY 901 TATAGCCCTGAGGAAACAAACCGCGCTGTTAAAGAGTAAAGAGTAAAGAGTAAAGTAA 960  
DB |||||  
QY 1380 TACAGCCAGAGGAGACGAGCGCGCTGTGAACAAAGTAAAGAGTAAAGAGTAAAGTAA 1439  
DB |||||  
QY 961 CTGAGCAGATAGGCGCTTAATCTTTCTGATGAGAGAGACGCCCGAGCAATTAATAC 1020  
DB |||||  
QY 1440 CTGAGCAGATAGGAGCAACCTCTTCTGATGAGAGAGACGTCAGAGCAATTAATAC 1499  
DB |||||  
QY 1021 CGGGTGTATTGGGCTCAGAACTGAGCTGCGAGTGAACATTTCTGTTCACTG 1080  
DB |||||  
QY 1500 CCGTGTATTGGGCGCAGAACTGAGCTGTGGCGTGGGACATCTGCAATCACCTC 1559  
DB |||||  
QY 1081 CTATTGTGATGCTCCGGGTGTTCAACTAGAACCTTCAGACCCCAATGTTATGGAGAAA 1140  
DB |||||  
QY 1560 TTGTTGTGATGCTCCGGGTGTTCCAGCTAGAACCTCCGACCCCATGCTATGAGAGAAA 1619  
DB |||||  
QY 1141 ACTTTAAGAAATTTGAGTGGAGTGTGTTCCAGAAATATCAGTAGCGTAGCTCA 1200  
DB |||||  
QY 1620 ACTTTAAGAAATTTGAGTGGAGTGTGTTCCAGAAATATCAGTAGCGTAGCTCA 1679  
DB |||||  
QY 1201 AGGATCAAGCTCCATCTCGTAACCACTCCAGAGTTTGTGTTCAAGCTGCAATCT 1260  
DB |||||  
QY 1680 AGAATCAAGCTCCATCTCGAACAACCTCCAGAGTTTGTCTCAGCGATGTCACACTGT 1739  
DB |||||

QY 1261 CATACATTGCTCATCTAGTACTTCTAGCTAGTTTCAGAAAAACAGCAATAAGATGAA 1320  
DB |||||  
QY 1740 CACACATTGCTCATCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 1799  
DB |||||  
QY 1321 GAGGAAACAGATGTCTCTATTGCTGTTGGCATGCTGTTGAAGAAAGTCTTACAGTG 1380  
DB |||||  
QY 1800 GAGGAGCAGATGTCTCTATTGCTGTTGGCATGCTGTTGAAGAAAGTCTTACAGTG 1859  
DB |||||  
QY 1381 TGTGAAGACGGCTGCGAGGAAACAGCTGCAACCACTGCTGATCTCAATTTGGGAGAGAG 1440  
DB |||||  
QY 1860 TGTGAAGACGGCTGCGAGGAAACAGCTGCAACCACTGCTGATCTCAATTTGGGAGAGAG 1919  
DB |||||  
QY 1441 TGTGAAGAAATAGAGAACTTTAATATGCTCCCTTTGATCTTAAGTGGAGATCTCAT 1500  
DB |||||  
QY 1920 TGTGAAGAAATAGAGAACTTTAATATGCTCCCTTTGATCTTAAGTGGAGATCTCAT 1979  
DB |||||  
QY 1501 GATTCTTACAGCAACAGCTGCTCAAGCTCTGCTGATCTCCCTTTCTCCCTCAGAGTCA 1560  
DB |||||  
QY 1980 GACTTCTACAGCAGCTAGCTTATCAAGCCCTGCTGATCTCCCTTACCTCCCTGCGAGTGA 2039  
DB |||||  
QY 1561 CAGCAGCAACCGTACAGCAGAGCTTTGGCTGGATCA--CGAAGGAATCAAGAGAG 1617  
DB |||||  
QY 2040 CAGCAGCTCTCTCCCGCAACAGCTGTGGCGGATCACGCGAGGAATCAGGAAGC 2099  
DB |||||  
QY 1618 AATTTTAACTTACTCATATGAACTCAGCAAACTCCCTCTCTGCTTACAAAGATTAGCT 1677  
DB |||||  
QY 2100 AATTTTAACTTACTCATATGAACTCAGCAAACTCCCTCTCTGCTTACAAAGATTAGCC 2159  
DB |||||  
QY 1678 GAGCAGTGAATTCAGGTTTGGAAATGGAATCTGCTGCTGCTTATTTCTAGAACTCG 1737  
DB |||||  
QY 2160 GAGCAGTGAATTCAGGTTTGGAAATGGAATCTGCTGCTGCTTATTTCTAGAACTCG 2219  
DB |||||  
QY 1738 AATGTGAGAGAGATGCGCTCTAGGCGCTCTTCCCATGATGTGCTGAGGCGCTCTGCTG 1797  
DB |||||  
QY 2220 AAGTAAAGGAGATGCGCTTAGGCGCTTTCCACGATGTTAGCGGCGCTCTGTTGTTG 2279  
DB |||||  
QY 1798 GCAAATGGGAGAGCAGCTGGAATTTCTGGGCGCAGCTGGAAGCAGCGCGAGTGGGGA 1857  
DB |||||  
QY 2280 GCGAACGGGAGAGCAGCTGGAATTTCTGAGCGGCGAGCGGAGGAGCCTTAAGTGTGCG 2339  
DB |||||  
QY 1858 GCCACAGTGGGTCTTCCAGACCACTATCTCAGAGAGATGTGCTGAGAGCAGCTGCTGAGC 1917  
DB |||||  
QY 2340 GCGCGCAGTGGGTCTTCCAGCGCCAGCATCTCAGGCGAGCTGTGGAGCGTCTCTGAGC 2399  
DB |||||  
QY 1918 GTTCTGTCAATGGTGTGCTGCTGACCTGTCTCAAAAGTGTAGTGTGCTGCTTTAAACAA 1977  
DB |||||  
QY 2400 GTCTGTCTATCGTGTGCGCTGACCTGTCTACAAAGTGTAGCTTGTCTTTAAACAA 2459  
DB |||||  
QY 1978 TTGAGAGCCATGCTGTATATATCTCTTCCAGCTAGTTTACGGAAGAAATCAAACTTCAG 2037  
DB |||||  
QY 2460 CTGAGAGCCATGCTGTATATATCTCTTCCAGCGCTGCGCAGAAAGAAATCAAACTTCAG 2519  
DB |||||  
QY 2038 AGACTTCTCAGCGAGTGTGAGACACCATCTCTAGTCAAAATGTGAGATGCCAATAGCCGC 2097  
DB |||||  
QY 2520 AGACTTCTCAGCGAGTGTGAGACACCATCTCTAGTGAAGTGGCAGACCCCAATAGCCGC 2579  
DB |||||  
QY 2098 ACAAGTCACTGTGCAATATCAACACTGTTGGAACCTGTGCAAGGCCCAAGCAGAGAGTTG 2157  
DB |||||  
QY 2580 ACAGTCACTGTGCAATATCAACACTGTTGGAACCTGTGCAAGGCCCAAGCAGAGAGTTG 2639  
DB |||||  
QY 2158 GCAGTTGGCAGAGAAATATCTAAAGCTGGATCCATTTGTTGTTGTTGTTGTTGTTGTTG 2217  
DB |||||  
QY 2640 GCAGTTGGCAGAGAAATATCTAAAGCTGGATCCATTTGTTGTTGTTGTTGTTGTTGTTG 2699  
DB |||||  
QY 2218 TTAAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2277  
DB |||||  
QY 2700 TTAAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2759  
DB |||||  
QY 2278 CTTTGTCTTATAGATGAGCTGTTGTTGGAATTTCTGCTGGAATTTTATCCTCATATGTC 2337  
DB |||||  
QY 2760 CTCTGTCTTATAGACAGATTGCTCTTGGAAAATTTCTGCGGAATTTTATCCTCATATGTC 2819  
DB |||||  
QY 2338 AGTACTGATGTTTCAACAGCTGAGCTGTTGAAATCAGGTATAGAGAGCTGCTGCTCCCTC 2397  
DB |||||

Db	2820	AGTACCAGTGTCTCAAGCCGAGCTGTGAAATCAGGTATAAGAGCTGTCTGCCCTC	2879
Qy	2398	TTAACCTTTTCTTGAGTCCCAATGTATATCCCACTCAATGGTTGGCAAACTTTCCAGA	2457
Db	2880	TTAGCCTTTGCCTTGCAATCCATTGCAATTCCTCTCTATGTCGGCAAACTCTCGGG	2939
Qy	2458	AGATCTACTTGTAGTTCGCAAGATGGTTACTACAGTACCCCATGTGTTTTCAAAAC	2517
Db	2940	AGATTTATCTGAGCTCAGACCAATGGTGACACAGTGCCTCCCTGTGTTTCCAGCTG	2999
Qy	2518	TTGAAATGTGTAGTGTTCCTCAGTTCACCTTCCCTCAGGATGCGTCCGTTTGATG	2577
Db	3000	GTAACCATGCTAAGTGTCTTGGATCTCTCCCACTTCGCCAGGATGCGCCGGCTCTGATG	3059
Qy	2578	GCTATTGCAGATGAGGTGGAATTTGCCGAGCCATCCAGTTGGCGCTAGACACACTTGG	2637
Db	3060	GCCATTCGACAGAGGTAGAAATGCGAGGTATCCAGCTGGGTTCCGAGACACTTTG	3119
Qy	2638	GATGGTCAACAGGACAGCTTTCTTGCAAGCACTGTTCCCAACAACATATCTGGAACCA	2697
Db	3120	GATGGCCAGCAGGACAG-CTCGCAGGCATTGGCCCTCCCGCTATC-----CA	3167
Qy	2698	GAGAACAGTTCCCTGAGTCACAGTCCATTATAGAGAAACTGGAAAGATTTATGTCT	2757
Db	3168	GAGAGCAGCTCCCTTGAGCACAAGCCATGTAGAGAAACTGGAAAGATTTAAAGCT	3227
Qy	2758	ACAAATTGATGCCAGTTTCAGAGGACATTCTTGAGAGACTGCGCAGCACTTCAGTAGA	2817
Db	3228	ACGAGACTGAGTGCAGCTCAGAGGACATTCTGACAGACTGGCTGGCGTTTCTGTAGGA	3287
Qy	2818	CTTCTAGTTCAACAAACAACAACAACACAGAGACAAACCAAGCCAAATGGTTCAA	2877
Db	3288	CTTCTAGTTCA-----GCAACAACAGACACAACAAGCCAAACAGTTCAA	3332
Qy	2878	ACAAAAGCAGACCCCAAGTCAGTGTGAACTCTCTCTCTTATCTCATCATTCCTCAA	2937
Db	3333	ACAAAAGCAGACCCCAAGTCAGTGTGAACTCTCTCTCTCTCTCTCTCTCTCTCTCT	3389
Qy	2938	TTAATGTTCCAGCCTTGTCACACCCCTTCTTCTCTACCCCATCTGTACAGCTGGCACT	2997
Db	3390	TTAATGTTCCAGCAATATCAGCCCCATGTTCTCTCTCTCTCTCTCTCTCTCTCTCT	3449
Qy	2998	GCAACAGATGTTCTAAGCATPAGACTTCAGGATTCATTCCTGCGAATACCTTCTGCA	3057
Db	3450	GTAACAGATGTTCTAAGCATPAGACTTCAGGCGTGTGTTCCCTCTGTAATATACCTCTG	3509
Qy	3058	TCTCTCAAAACACAGCGCAAGTTTCTCTCAAAATCCACAGAACTGCTCTGAAACAA	3117
Db	3510	TCTCCCCAAACACAGCGCAAGTTTCCCTACAGTTCACAGGACCTGCTCTGAGAACCGA	3569
Qy	3118	GACTCAGATAAATTTTCCAGTGTCTTCTCAGTCAAGACCTTTGCCCTCCAGTAACATA	3177
Db	3570	GACTCAGAAAAAATCTCCCCAGTCTTACTCAGTTCGAGACCCCCACCTCCAGTAACATA	3629
Qy	3178	CACAGGCCAAAGCCATCTAGACCTACCCAGGTAAATCAAGTAAACAGGAGAGTCCCTCA	3237
Db	3630	CACAGGCCAAAGGCATCCGACCCGTTCCGGGTAGCAGCAAACTAGGGGATGCTCA	3689
Qy	3238	AAAAATAGCATGACACTTTTCCAGTGTCTTCTCAGTGTGAAACCTTTGCCCTCCAGTAACATA	3297
Db	3690	AAAAACAGCATGACACTCGACCTGAACAGTGTCTTCCAGTGTGATGACAGCTTTGGCAGT	3749
Qy	3298	AGCAGCAATAGTAGTAATGCTGTATACCCAGTCACGACAGTGTTCACCCCAAGTAGAG	3357
Db	3750	GGCAGCAACAGTGGCAGCGCGCTCATACCCAGTGGAGAGCGGCAATTCACCCCAAGTAGAG	3809
Qy	3358	GAGAAATCGATGATGTGATGATCAATACAGAGCTCAACTCCAGTATTTAGGACCTTCTGAA	3417
Db	3810	GACAGTGCAGGTAGATGTCAACCCGAGTCAACTCCAGTATTCGAGGACCTTCTTGA	3869
Qy	3418	GCATCTATGCCCTTCAAGTGATACAAACAGTAACTTTTAAAGTCAGAGGTTGTGTCTCTCT	3477

Db	3870	GCATCTATGCGCTTCAAGTGCACAAACAGTCACTTTTCAAGTCCGAAGTCCGCCGCTCTCTCT	3922
Qy	3478	CCTGAAAGGCGTGAATAATGATGATACCTCAAAAGATGATGTGAATCATATCAATAAAGTGC	3537
Db	3930	CCTGAGAAGCGCGAAGTGAATGACACCTACAAAGATGACGCTCAATCACAATCAAAAGTGC	3989
Qy	3538	AAAGAGAGATGGAAGCTGAAGAGAGAAAGCTTTTAGCAATTGCCATGCGCAATGTGCAGCG	3597
Db	3990	AAAGAGAAGATGGAGGCTTGAGAAAGAGAGCGGCTCCGATTTGCCATGGCAATGTGGCT	4049
Qy	3598	TCTCAGGATGCCCTCCCATAGTTCCTCAGCTGCAGGTTGAAAATGGAGAAGATATCATC	3657
Db	4050	TCTCAGGACGCCCTCCCCATAGTCCCTCAGCTGCAGGTGGAATGGAGAGGATATCATC	4109
Qy	3658	ATTATTCAACAGGATACACCAAGACCTCTACCAGGACATACCAGGACAAACCAACCGTAT	3717
Db	4110	ATCATCCAGCAGGATACACCAAGAACCTTACCAGGGCATCAAGCGACGAGCCTTAC	4169
Qy	3718	AGAGAAGACATGAATGGCTGAAAGGTCAACAGATAGGCCCTTGAGAGCAATTTTCTCTGT	3777
Db	4170	AGAGAAGACACCGATGGCTGAAAGGGCAGCAGATAGGCCCTCGGAGCAATTTTCTCTGT	4229
Qy	3778	TATCAGGCTCAAGATGTGGGAACCTGGAACCTTTAATGGCTGTAAACAGGTGACTTATGTC	3837
Db	4230	TACCAGGCACAGGATGTGGGCACCTGGAACCTTAATGCTGTGAAACAGGTGACCTACGTC	4289
Qy	3838	AGAAACACATCTTCTGACCAAGAAAGTATAGAACCATAGAGAAGAGATAGAATG	3897
Db	4290	AGAAACACATCTTCTGACGAGGAGAAAGTGGTGGAGGCCCTTGAGGGAAGAGATCAGGATG	4349
Qy	3898	ATGAGCCATCTGAAATCATCCAAAATCATTAGGATGTGGGAGCCACGTTGAGAAGAGC	3957
Db	4350	ATGAGCCACCTCAACCATCCGAAATCATCAGGATGTGGGGGCCACGTCGAGAAGAGC	4409
Qy	3958	AATTACAATCTCTTCAATGAATGATGGCAGGGGGATCGTGGCTCATTTGCTCAGTAAA	4017
Db	4410	AACTACAACCTCTTCAATCGATGATGGCGGAGCCCTCCGTGGCTCACCTTTCAGTAAA	4459
Qy	4018	TATGAGCGCTTCAAGAAATCAGTAGTATTAACTACACATGAAACAGTTACTCCGTGGCCTT	4077
Db	4470	TATGAGCTTTCAAGGAGTCACTGGTCAATTAACATACACAGACGAGTTACTCCGTGGCCTT	4529
Qy	4078	TCGTATCTCCATGAANAACCAATCATTCACAGAGATGTCAAAGGTGCCAATTTCTCTAAT	4137
Db	4530	TCCTATCTCCAGGAACCAATCATTCACAGACGTCAAAGGGGCCAATCTGCTCAT	4589
Qy	4138	GACGACACTGTGTCAGACACTAAGAAATTCAGATTTTGGAGCTGCAGCCAGTTGGCATCA	4197
Db	4590	GACAGCACCGGTCAAGCGCTCAGAATTCAGACTTCGGTGTGTCGCCGCGAGTTGGCATCC	4649
Qy	4198	AAAGGAATGTGTGCAGGAGAGTTTCAGGGACAATTTACTGGGGACAATTCATTTATGGCA	4257
Db	4650	AAAGGAATGTGTGCAGGAGAGTTTCAGGGACAATTCATTCGGGGACAATTCATTTATGGC	4709
Qy	4258	CCTGAGGTACTAAGAGGTCACACGATPAGGAAGGAGCTGTGATGTATGGAGTGTGGCTGT	4317
Db	4710	CCTGAGGTACTAAGAGGTCACACGATPAGGATTCAGGAGCTGTGACGCTTCGAGTGTGGCTGC	4769
Qy	4318	GCTATTATGAATAATGGCTGTGCAAAACCAATGGGAATGCAGAAAAACACTCCCAATCAT	4377
Db	4770	GCAATTATGAATAATGGCTGTGCAAAACCACTTGGGAACGCAAAAGCACTCCCAATCAT	4829
Qy	4378	CTTGCTTTGATATTTAAGATGCTAGTGCACACTACTGCTCAATCGATCCCTTTCACATTTG	4437
Db	4830	CTTGCTTTGATATTTAAGATGCGAGTGCACACTACTGTCACCATCCATCCCGTTCACCTG	4889
Qy	4438	TCTCTGTGTTTACGAGATGTGCTCTCTGTTGTTTATAGAACTTCAACCTCAGGACAGACT	4497
Db	4890	TCCCCGGGCTTCGAGACGTTGGCTCTGCGCTGTGTTTATAGAACTTCAACCTCAGGACAGACT	4949
Qy	4498	CCATCAAGAGAGCTACTGAAGCATCCAGTCTTTTGTGATCAATATGGTAGCCAAATATGCAG	4557
Db	4950	CGGTCAAGAGAGCTACTGAAGCATCTCTGTTTCCGTCAACATGATGATGTAACCTT	5003

QY 4558 ATCAACTACAGTAAACAGGAGTGTCAACAGAGAGAAAAAACTTGTGGGACACAT 4617  
Db |||||  
5004 -----GCTCAGGGTGGCAACAG-GAAGAGAACTCGGGGACACAGT 5048  
QY 4618 TGATATCTTACTGGCCATGATGCACTGAACAGCTATGAACGAGCCAGTGGGAAACCT 4677  
Db |||||  
5049 TGATAGTGTGTGCTGCTTATACCACTGACCCAG-----AAGAGGGGCCAGTGGGAGCCCG 5103  
QY 4678 TACCTAAGTATGTGATTGACAAATCATGATCTGTACCTTAAGCTCAGTATGCAAAAGCCCA 4737  
Db |||||  
5104 CACTTAAGCATGTGACTGACAAATCATGA-CTGCACCTGAGCTCCGCTCTGACAGGGCTA 5162  
QY 4738 -AACTAGTGCAGAACTG 4754  
Db |||||  
5163 CAACCTGTGAGGAGCTG 5180

## RESULT 9

ADB53534  
ID ADB53534 standard; DNA; 5180 BP.

AC ADB53534;

XX

XX

DT 04-DEC-2003 (first entry)

XX

XX

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4076.

XX

KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;

KW toxicity marker; toxicity progression; drug screening;

KW primary rat hepatocyte toxicity modelling; gene; ds.

XX

OS Rattus norvegicus.

XX

PN WO2003065993-A2.

XX

PD 14-AUG-2003.

XX

PF 04-FEB-2003; 2003WO-US003482.

XX

PR 04-FEB-2002; 2002US-0353171P.

PR 13-MAR-2002; 2002US-0363534P.

PR 08-APR-2002; 2002US-0370248P.

PR 10-APR-2002; 2002US-0371134P.

PR 10-APR-2002; 2002US-0371135P.

PR 10-APR-2002; 2002US-0371150P.

PR 11-APR-2002; 2002US-0371413P.

PR 19-APR-2002; 2002US-0373602P.

PR 22-APR-2002; 2002US-0374139P.

PR 08-MAY-2002; 2002US-0378370P.

PR 09-MAY-2002; 2002US-0378652P.

PR 09-MAY-2002; 2002US-0378653P.

PR 09-MAY-2002; 2002US-0378655P.

PR 09-JUL-2002; 2002US-0394230P.

PR 09-JUL-2002; 2002US-0394253P.

PR 04-SEP-2002; 2002US-0407688P.

PR 28-JAN-2003; 2003US-0442900P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Mendrick D, Porter M, Johnson K, Higgins B, Castle A, Orr M;

PI Elashoff M;

XX

DR WPI; 2003-731472/69.

XX

PT Determining if a compound induces a toxic effect on a tissue or cell, for

PT identifying hepatotoxic compounds, comprises comparing a gene expression

PT profile of a tissue or cell sample to a database of tox mean and non-Tox

PT mean values.

XX

PS Claim 44; SEQ ID NO 4076; 874bp; English.

XX

CC The present invention describes a method for determining whether a  
CC compound induces a toxic effect on a tissue or cell. The method comprises  
CC preparing a gene expression profile of a tissue or cell sample exposed to  
CC the compound, and comparing the gene expression profile to a database  
CC comprising data or information on the tox mean and non-tox mean value.  
CC The method is useful for predicting or identifying at least one toxic  
CC effect, particularly hepatotoxicity, of a test or unknown compound. The  
CC genes listed in the specification are useful as diagnostic or toxicity  
CC markers for the prediction or identification of the physiological state  
CC of tissue or cell sample that has been exposed to a compound, or to  
CC identify or predict the toxic effects of a compound or an agent. These  
CC may also be used as markers for monitoring toxicity progression or for  
CC drug screening. The present sequence represents a primary rat hepatocyte  
CC toxicity modelling related gene sequence from the present invention.

XX  
XX Sequence 5180 BP; 1225 A; 1521 C; 1443 G; 991 T; 0 U; 0 Other;

Query Match 65.2%; Score 3420.8; DB 9; Length 5180;  
Best Local Similarity 84.5%; Pred. No. 0;  
Matches 4020; Conservative 0; Mismatches 647; Indels 91; Gaps 12;  
QY 1 GAGAAAATGGCGCGCGCGCGGGAATCGCGCTCTGTCGGGATTCGCGGCCAGG 60  
Db |||||  
510 GAGAAAATGGCGCGCGCGCGCGGATCGCGCTCTGTCGGGATTCGCGGCCAGG 569  
QY 61 GCTACAGCCCTGAGCGAGCGCGCGCGGAGGAGCCCTCAAGGCGAGCGCGCGCG 120  
Db |||||  
570 GCGGGGAGCGCGCGCGCGCGCGCGGAGGAGCTCTCCAGGAGGCGCGCGCGCGCA 629  
QY 121 GCTGCCGCGCGGACTGTCGCGGAGCGCGGCGCGGAGCGCGGCGCGGAGTGGCGG 180  
Db |||||  
630 GCGGGCGCGGGGCTGCTGCGGGAGACTGGCAGCGCGGGCGCGGAGCGGACTGGCGG 689  
QY 181 CGGCGGAGCTGCGGAAAGTGGGAGTGTGGAGCTGGAGCCAGCTGCTGAGCAGCGCTC 240  
Db |||||  
690 CGGCAGCAGCTGCGGAAAGTAAAGAGTGTGGAGCTGGAGCCAGCTGCCGAGCAGCGCTC 749  
QY 241 TTCCTTGCCGCTCAACCGCGCGCTCTCTGACTTCCCGCTCGCGGAGCGCGCGAGCGCA 300  
Db |||||  
750 TTCCTCACCGCTCGCGCGCTGCGCCATCTACTTCCCGCTCGCGGAGCGCGCGAGCGG 809  
QY 301 GCGGGAGTGGGACCGGCTTCAGCGCTGTGGCGGTGCGCGCGCGCGCGCGCGCGAGC 360  
Db |||||  
810 GCTGCAGGAGCGAGTGGCTTCAGCGCTGCGCGGAGCGCGCGCGCGCGCGAGCGAGT 869  
QY 361 CG 420  
Db |||||  
870 CGCTGCGGCTCCCATCTCTGCGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 929  
QY 421 GCAGCG 480  
Db |||||  
930 GCGGGG-----GCGGAGCGCGCGCTCTCTGCGCGCGCG 959  
QY 481 CCGCGCGCTGCTGAGATGGAGAACTCTCAAGGGTTGCAAGAGATGGATGAT 540  
Db |||||  
960 CCTCCGCTGAGAGATGGAGAACTCAAGAACTCAAGAGATGGATGATGATGATGATGAT 1019  
QY 541 CGTCCAGAGGAAAGATGATGAGGAGAACTGAAAGGCAACCTGATGCGACCGCTGGAG 600  
Db |||||  
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QY 601 CACGATGTTGGAAGGAGAAATAGGCGAGGCGCTGTGGTGAATTAACCAATCCAGTT 660  
Db |||||  
1080 CACGATGTTGGAAGGAGAAATAGGAGAGGCGCTGTGGTGAATTAACCAATCCAGTT 1139  
QY 661 AAAGGAGATGGATCTGAAATGAATCACTTACAGCTGAGTCTCCAGGAGAGTCCAGGCA 720  
Db |||||  
1140 AAAGGAGATGGATCTGAAATGAATGATTAACCTCAAGAGATGGATGATGATGATGATG 1199  
QY 721 AGTGGCGCTTACAGCTTCCAAAGCGAGCGAGCTCTTCTTCTTCTTCTTCTTCTTCTT 780  
Db |||||  
1200 GGCTCTGCTGACACAGCTCCCAAGGGCGCGAGAGCGCGCTCTCTTGAAGAGTCCCATCA 1259



3390	TTAATGTTTCCAGCAATATACAGCCCAATGTTCACTGCGCCCGTCTGTCCACAGCTGGCTCT	3444
2998	GCAACAGATGTCCTAAAGCATAGACTTCAGGGAATCATTTCCCTGCGAATAACCTTCTGCA	3057
3450	GTAAACAGATGCTCTTAAGCATAGACCTCGCGCGTGTGTTTCCCTGTATAATACCCCTCTGG	3509
3058	TCTCCTCAAAACAGCGCAAGTTTCTCTACAATTCACAGAAACTGTCTCGTGAACAACA	3117
3510	TCCTCCCAACAACAGCGCAAGTTTCCCTACAGTTCAGAGAGACCTGCTCTGAGAACC	3569
3118	GACTCAGATAAACTTTTCCCGAGTCTTTACTCAGTCAAGACCCCTTGGCCTCCAGTAACATA	3177
3570	GACTCAGAAAAAATCTCTCCCGAGTCTTTACTCAGTTCAGACCCCAACCCCTCCAGTAACATA	3629
3178	CACAGGCCAAAGCCATCTAGACCTACCCCAAGTAAATACAAGTAAACAGGAGAGATCCCTCA	3237
3630	CACAGGCCAAAGCATCCCGACCCGTTCCCGGTAGCACAGCAAACTAGGGGATGCTCA	3689
3238	AAAAATAGCATGACACTTGTATCTGTGAACAGTAGTTTCAAATGTGATGACACTTTGGCTGT	3297
3690	AAAAACAGCATGACACTCGACCTGAACAGTGTCTTCCCAAGTGTGATGACACTTTGGCAGT	3749
3298	AGCAGCAATAGTAGTAATGCTGTATATACCAGCATGACGAGACAGTGTTCACCCCAAGTAGAG	3357
3750	GGCAGCAACAGTGGCAGCGCGTCATACCCAGTGAGGAGACGGCAITTCACCCAGCAGAG	3809
3358	GAGNAATGCAGATTAGATGTCAATACAGAGCTCAACTCCAGTATTGAGGACCTTCTTGAA	3417
3810	GACAAGTGCAGGTTAGATGTCAACCCCGAGCTCAACTCCAGTATCGAGGACCTTCTTGAA	3869
3418	GCATCTATGCCCTTCAAGTGATACAAACAGTAACATTTTAAAGTCAGAAGTGTGCTGCTGTCT	3477
3870	GCATCTATGCCCTTCAAGTGACAAACAGTCACATTTCAAGTCCGAAGTCGCGCTCTCTCT	3929
3478	CCTGAAAAGGCTGAAATGATGATACCTACAAAGATGATGTGATCATATATCAAAAGTGC	3537
3890	CCTGAGAAGGCCGAAAGTGATGACACCTACAAAGATGACGTCAATCAATCAAAAGTGC	3899
3538	AAAGAGAGATGGAAGCTGAAGAGAAGAAGCTTTAGCAATTTGCCATGGCAATGTCCAGCG	3597
3990	AAAGAGAGATGGAAGCTGAGGAAGAGAGGCGCTCGCGATTGCCATGGCAATGTCCGGCT	4049
3598	TCTCAGATGCCCTCCCATAGTTCTCTCAGCTGCAGGTTGAAATGAGAGAGATATCATC	3657
4050	TCTCAGAGCGCCCTCCCATAGTCCCTCAGCTGCAGGTGGAATGAGAGAGATATCATC	4109
3658	ATTATTCAACAGGATACACCAAGACACTACAGGACATACCAAGCAAAACCAACCGTAT	3717
4110	ATCATCCAGCAGGATACACCAAGAAACCTTACAGGGCATACCAAGCGAACGAGCCCTAC	4169
3718	AGGAGACACTGAATGGCTGAAAGGTCAACAGATGGCCTTGAGACATTTCTTCTGT	3777
4170	AGAGAGACACCGAGTGGCTGAAAGGGCAGCAGATAGCCCTCGGAGCATTTTCTTCTGT	4229
3778	TATCAGGCTCAAGATGTGGGAACCTGAACTTTAATGGCTGTAAACAGGTGACTTATGTC	3837
4230	TACCAAGCACAGGATGTGGGCACCTGGAACTTTAATGGCTGTGAAACAGGTGACCTACGTC	4289
3838	AGAAACACATCTTCGACAGAGAGAGTAGTAGACACTTAAGACAGAGAGAGATAGAGATG	3897
4290	AGAAACACATCTTCGACAGAGAGAGTAGTGTGAGCCCTTGAGGAGAGATCAGGATG	4349
3898	ATGAGCCATCTGAATCATCCAAAACATCATTTAGGATGTTGGAGGCCAGCTGTGAGAAGGC	3957
4350	ATGAGCCACCTCAACCATCCGAAACATCATCAGGATGCTGGGGGCCACGTCGAGAAGAGC	4409
3958	AAATTACATCTCTTCATGTGATGATGGCAGGGGATCGGTGGCTCATTTTCTGAGTAAA	4017
4410	AACTACAAACCTCTTCATCGAGTGTGATGGGGAGCCTCCGTGGCTCACTCTTGAGTAAA	4469
4018	TATGGAGCCTTCAAGAAATCAGTAGTTATTAACATACACTGAACAGTAGTTACTCCGTGGCCTT	4077
4470	TATGGAGCTTCAAGAGAGTCACTGGTGTATTAACATACAGAGCAGTAGTTACTCCGTGGCCTT	4529

Qy	4078	TCGTAATCTCCATGAAGAACCAAAATCAATTCACAGAGATGTCAAAGGTCGCCAATTTGCTAAATT	41337
Db	4530	TCCTATCTCCACGAGAACCAAGATCATTTACAGAGACGTCAAAGGGGCCAAATCTGCTCATTT	4589
Qy	4138	GACAGCACTGGTCAGAGAGCTAAGAAATTCAGATTTTGGAGCTCGAGCCAGGTTGGCATCA	4197
Db	4590	GACAGCACCGGTCTAGCGGCTCAGAAATTCAGAGCTTCGGTGTCTCCGCCAGGTTGGCATCC	4649
Qy	4198	AAAGGAATCTGGTCAGAGAGAGTTTTCAGGGAACAATTAATTCGGGGAACAATTCGATTTATGGCA	4257
Db	4650	AAAGGAATCTGGTCAGAGAGAGTTTTCAGGGAACAGTTACTGGGGAACAATTCGATTTATGGCG	4709
Qy	4258	CCTCAGGTACTTAAGAGTCAACAGTAGTGAAGAGAGCTGTGATGTATGGAGTGTGGTCTGT	4317
Db	4710	CCTCAGGTACTTAAGAGTCAACAGTAGTGAAGAGCTGTGACGTCTGGAGTGTGGTCTG	4769
Qy	4318	GCTATTATGAAGATGGCTTGTGCAAAACCAACCTGGGAATCGAGAAACCACTCCAATCAT	4377
Db	4770	GCCATTATGAAGATGGCTTGTGCAAAACCAACCTGGGAACGAGAAAGCACTCCAATCAT	4829
Qy	4378	CTTCGTTTGTATTTAAGATTGCTAGTGCACACTACTGCTCATCGATCCCTTCACATTTG	4437
Db	4830	CTTCGTTTGTATTTAAGATTGCGAGTGCAACTACTGTCACATCCATCCCGTCACACCTG	4889
Qy	4438	TCTCCTCGTTTACAGAGATGGCTCTTCGTTGTTTGAACCTTCAACCTCAGGACAGACCT	4497
Db	4890	TCCCGCGGCTCGAGACGTGGCTCTCGCTGTATTAGAACTTCAACCTCAGGACAGACCT	4949
Qy	4498	CCATCAGAGAGCTACTGAAGACTCCAGTCTTTTCGTACTACATGGTAGCCAAATATGACG	4557
Db	4950	CCGTCAAGAGAGCTACTGAAGACTCCCTGTCTTCGTACAACATGGTAGTCAACT-----	5003
Qy	4588	ATCAACTACAGTAGAAGAACAGGATGCTCAACAGAGAAAAAAAACCTTGTGGGAAACCAAT	4617
Db	5004	-----GCTCAGGGTCGCAACAAG-GAAAGAAAACTCGCGGCGAGCCACGT	5048
Qy	4618	TGATATTCTACTGCGCATGATGCCACTGAACAGCTATGAACGAGGCCAGTGGGGAACCTT	4677
Db	5049	TGATAGTCTGTGTGCC--TCATACCACCTGACCAAG-----AAGAGGGGCCAGTGGGAGCCCG	5103
Qy	4678	TACCTTAAGTATGTGATTGACAAAATCATGATCTGTACCTTAAGCTCAGTATGCAAAAAGCCCA	4737
Db	5104	CACCTAAGCATGTGACTGACAAATCATGA-CTGCACCTGAGTCCGTCTGCAGACGGCTA	5162
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Db	5163	CAACTCGTCAGGAGCTG	5180

RESULT 10  
AAX80911  
ID AAX80911 standard; cDNA; 5253 BP.

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FT		/*taq= b

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FT /product= "MEK1 protein"
FT /function= "Regulates cellular apoptosis"
FT mat_peptide 2637..4493
FT /*tag= d
FT /note= "Active fragment that mediates apoptosis"
FT 3'UTR 4497..5253
FT /*tag= C
FT
FT XX WO9941385-A1.
FT PD 19-AUG-1999.
FT XX
FT PF 12-FEB-1999; 99WO-US002974.
FT XX
FT PF 13-FEB-1999; 98US-00023130.
FT XX
FT PA (CADU-) CADUS PHARM CORP.
FT XX
FT FI Johnson GL;
FT XX
FT DR WPI; 1999-508649/42.
FT DR P-PSDB; AAY26234.
FT XX
FT PT A new mammalian serine-threonine protein kinase for treating disorder
FT PT characterized by aberration of the enzyme gene.
FT XX
FT PS Claim 1a; Page 113-119; 149pp; English.
FT CC
FT CC The present sequence is an isolated murine MEK1 cDNA. It encodes Mitogen
FT CC ERK Kinase Kinase 1 (MEK1) protein, which functions to integrate
FT CC proteases and signal transduction pathways involved in the regulation of
FT CC apoptosis. It is a 196 kDa protein kinase, which upon cleavage at Asp
FT CC 871/874 by caspase Generates a 91 kDa kinase fragment that induces
FT CC apoptosis and a 113 kDa NH2-terminal fragment. Mutant MEK1 proteins that
FT CC are resistant to cleavage by caspase proteases and capable of inhibiting
FT CC apoptosis can be produced. MEK1 proteins and antibodies immunoreactive
FT CC with MEK1 are used in diagnostic and therapeutic assays and reagents for
FT CC detecting and treating disorders involving aberrant expression or
FT CC activation of the MEK1 gene products. DNA probes or primers that
FT CC selectively hybridize to MEK1 cDNA, can be used for its detection in
FT CC samples
FT XX
FT SQ Sequence 5253 BP; 1299 A; 1403 C; 1433 G; 1118 T; 0 U; 0 Other;
FT
FT Query Match 65.1%; Score 3417; DB 2; Length 5253;
FT Best Local Similarity 83.5%; Pred. No. 0; Mismatches 705; Indels 101; Gaps 14;
FT Matches 4081; Conservative 0;
FT
FT QY 1 GAGAAATGGCGGCGGCGGGAATCGGCTCGTCTCGGATTCGCGGCGCCAGG 60
FT Db 9 GAGAAATGGCGGCGGCGGCGGATCGGCTCGTCTCGGATTCGCGGCGCCGCG 68
FT
FT QY 61 GCTACGAGCCCTGAGCAGCGCGCGC-----GGAGGAGCCCTCAAGCGGAGCG 111
FT Db 69 GCGGCGAGTCCCGAGCGGCGGCGGCGGCGGAGGAGGAGGAGTCTCCAGGGAAGCGCG 128
FT
FT QY 112 GCGCC---GCGGCTCGCGGAGCTGCTCGGAGCGGCGGCGGCGGCGCGGCGG 168
FT Db 129 GCGCCCGCAGCGGCGGCGGCGGCGGCTGCTCGGAGCCCTGGCAGCGCGGCGGCGG 188
FT
FT QY 169 GCGGACTGGCGGCGGCGGAGCTGCGCAAGTCGCGAGTGTGAGTGAACAGCTGCT 228
FT Db 189 GCGGACTGGCGGCGGCGGACGTCGCGCAAGTCGCGAGTGTGAGTGAACAGCTGCT 248
FT
FT QY 229 GAGCAGCGCTCTTCTTTCGCGCTCAGCGCGCGCT---CTCGACTTTCGCGCGCG 285
FT Db 249 GAGCAGCGCTCTTCTTTCGCGCGCGCTCAGCGCGCTTCTTCTTCTTCTTCTT 308
FT
FT QY 286 GAGCGCGGAGCGGCGGAGTGTGGAACCGGCTTCAGCGCTGTGCGGCGGCGCGCG 345
FT Db 309 GAGCGCGGAGCGGCTGTGAGGAGGAGTGTGCGCTTCCAGCGCGGCGGCGGCGG 368
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QY 346 CACGAGCGCGGCGGCGGCGCCACCTTACCGAGTCGGTGGCGCGCGCGACAGC 405
Db 369 CCGGAGCGCGGAGTCGCTGCGGCTCCCACTCTGCGAGCTGGCGCGCGCGGACAGC 428
QY 406 GCGCGCTCGAGTCCCGCAGCGCGCGAGCCCGGGGAGAAAGCGCGCGCGCGCGCGG 465
Db 429 GCGCGCGGAGCGCGCGCGGG-----GCGGAGCGG 458
QY 466 TCTCTGCGAGCGCGCGCGCGCGTCTGAGATGGAGAAATAAGAAACTCTCAAGGGTTG 525
Db 459 CCTCTGCGAGCGCGCGCGCGCTCGGTGAGAGATGGAGAAATAAGAAACTCTCAAGGACTG 518
QY 526 CACAAGATGGATGATGCTCCAGAGAAAGATGATCAGGAGAAACTGAAGCAACCTGT 585
Db 519 CACAAGATGGAGATCGCGCGGAGGAGAAATGATCCGGGAGAACTCAAGCGACCTGT 578
QY 586 ATGCCAGCTCGAAGCAGCAATGGTTGGAAGAGAGAAATAGCGAGGCGCTGTGTGGTGA 645
Db 579 ATGCCGCGCTGGAAGCAGCAATGGTTGGAAGAGAGAAACAGGAGAGCGCTGTGTGGTGA 638
QY 646 AAACCAATCCAGTTAAAGGAGATGATCTGAAATGAATCACTTAGAGCTGAGTCTCA 705
Db 639 AAGCCCAATCCCTATTAAAGGAGATGATCTGAAATGAATCACTTAGAGCTGAGCGCCAG 698
QY 706 GAGAGGTCCAGCAAGTCGCGCTTACCAGCTTCCAAAGGCGCGAGCGAGTCTTCTCT 765
Db 699 GGAGAGGCGCAGCAGGTTCGCTGCACCGCCCCCAGGCGCGAGAGCGCCATCTCT 758
QY 766 GGCACCTCCCGCTCAGGTGCGCAAGTGAATCAGAAATCTCCAGGAGTAAAGAGAAAGA 825
Db 759 GGCAGCTCTCCGTCAGGCGCTCGGTGAAGCGGAAATCCCGAGGAGTAAAGCGAAACA 818
QY 826 GTTTCGCCAGTGCCTTTTCAGAGTGGCAGAAATCACACACCCCGAGAGCGCCCTTCA 885
Db 819 GTGTCCCGGCTGCTTTTCAGAGTGGCAGAAATCACACACCCCGAGAGCGCCCTTCA 878
QY 886 GATGGCTTCTCACATATATAGCCCTGAGGAAACAAACCGCGGTGTAAACAAGTGTGCGG 945
Db 879 GATGGCTTCTCCCGTACAGCCCGCAGAGGAGAGAGCGCGCGCGGTGAACAAGTGTAGA 938
QY 946 GCACAGTGTACTTACTGAGCAGAGTGGCGCTTCTCTCTGATTCGAGGAGAGCAGC 1005
Db 939 GCCAGGCTGTACTGCTGAGCAGATAGGACCACTCTTCTGATTCGAGGAGAGCAGT 998
QY 1006 CCAGACATAAATACCGGCTGTTTATTTGGGCTTCAGAACTGCAGCTGTGCACGTGGAACA 1065
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QY 1066 TTCTGTATTCATCTGCTATTTGTGATGCTCCGCGGTGTTCACTAGAACTTCAGACCCA 1125
Db 1059 TTCTGTATTCATCTGCTATTTGTGATGCTCCGCGGTGTTTCAGCTAGAACCCCTCTGACCCC 1118
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QY 1186 AGTAGGCGTATGCTCAAGGATCAAGCTCCATCTGCTTAAACCATCCAGAGTTTGTTC 1245
Db 1179 AGTAGGCGTATGCTCAAGATCAAGCTCCATCCCGGAAACCATCCAGAGTTTGTTC 1238
QY 1246 GCGATGTCAAATCTCTCATATCTGTATCATCTAGTACTTCTACTGCTAGTTCAGAAAAAC 1305
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Db 1299 AGCATGAAGATGAAGAGGAGCAGATGTGTCTTCTGTTGTTGGCATGCTTGATGA 1358
QY 1366 GAAAGTCTTACAGTGTGGAAGCGGCTGCAGGAAACAAAGCTGCACACCACTGCATGTCA 1425
Db 1359 GAGAGCTGACTGTGTGTGAGAGTGTGCTGCAGGAAACAAAGCTGCACCACTGCATGTCC 1418
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QY 1426 ATTTGGCAGAGAGTGTAGAGAAATAGAGAACTTTAATATGTCTCCCTTTGTAGATCT 1485  
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QY 1486 AAGTGGAGATCTCATGATTTCTACAGCAGAGTGTCAAGTCTGTGGATTCCCTTCT 1545  
DB 1479 AAGTGGAGATCCCATGATCTCTACAGCCATGAGTATCAAGCCCGGTGGAGTCCCGGCC 1538  
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QY 1663 TACAAAGATTTAGCTGAGCCATGATTCAGTGTGTTGGAAATGGAATCGTGTGGCTGCTTA 1722  
DB 1659 TACAAAGATTTGGCCGAGCCATGATTCAGTGTGTTGGAAATGGAATCGTGTGGCTGCTTA 1718  
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QY 1843 AGCCGAGTGGGAGGACACAGTGGGTCTTCCAGACCAAGTATCTCAGAGAGTGTGGT 1902  
DB 1839 AGCTTAAAGCGGGAGGCGGAGCGGGTCTCCAGCCAGCCAGCATCTCAGGGGATGTGGT 1898  
QY 1903 GAGCATGCTCAGCGTCTCTCAATGTCTGCTGCTGACCTGCTCTACAAAGTGTAGCTT 1962  
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QY 2143 CAAGCAGAGAGTGGCAGTGGCAGAGAAATATCAAGCTGATCCATGTTGTTGGT 2202  
DB 2139 CAAGCAGAGAGTGGCAGTGGCAGAGAAATATCAAGCTGATCCATGCGGGTGGT 2198  
QY 2203 GGTGTTGATTATGCTTAAATGTTATCTTGGAAACCAAACTGAATCAAACTTGGCAA 2262  
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DB 2499 GTGTTTCAAACTGTTAGAAATGCTTAAATGCTTCTGGCTCCACCACTTCCACAGATG 2558  
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DB 2949 GTCC-----CAGATATTCTTAAGCAGACAGCCAGGCTTTGTTCCCTGC 2993  
QY 3043 AGAATACCTTCTGATCTCTCTCAACAGAGCGCAAGTTTCTCTACAAATTCACAGAAAC 3102  
DB 2994 AATATACCTTCCGCTCTCTCAGACAGCGCAAGTCTCTCTCAAAATTCAGAGGAC 3053  
QY 3103 TGTCTGAAACAAAGACTCAGATAAATTTCCCGAGCTTTTACTCAGTCAAGACCTGTG 3162  
DB 3054 TGCTCTGAACACGAGACTCAGACAGCTCTCCCGAGTCTTCTCAGTCAAGACCCCA 3113  
QY 3163 CCTCAGTAAATACACAGGCGCAAGCATCTAGACCTACCCAGGTAAATACAGTAA 3222  
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QY 3223 CAGGAGATCCCTCAAAATAAGCATGACACTTGTATCTGAACAGTAGTTCCAAATGTGAT 3282  
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QY 3283 GACAGCTTTGGCTGTAGCAGCAATAGTAGTAATGCTGTTATACCAGTGAACAGAGT 3342  
DB 3234 GACAGCTTTGGCGGCGCGCAACAGTGGCAACGCGCTCATACCAGGAGCAGAGAGT 3293  
QY 3343 TTCACCCAGTAGAGAGAAATGCGATTTAGATGTCAATACAGAGCTCAACTCCAGTAT 3402  
DB 3294 TTCACCCCGGTGAGAGCAAGTGTAGTGTAGATGTGAACACAGAGCTCAACTCCAGATC 3353  
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Qy 3763 GCATTTCTCTCTGTTATTCAGGCTCAAGATGCTGGAACTGTTAAATGGCTGTTAAA 3822  
Db 3714 GCATTTCTCTCTGTTATTCAGGCTCAAGATGCTGGAACTGTTAAATGGCTGTTAAA 3773  
Qy 3823 CAGGTGATATATGTCAGAAAACATCTTCTGAGCAAGAGAGTGTAGAGACACTAAGA 3882  
Db 3774 CAGGTGATATATGTCAGAAAACATCTTCTGAGCAAGAGAGTGTAGAGACACTAAGA 3833  
Qy 3883 GAAGAGATAAGATGATGAGCCATCTGAATCATCCAAACATCATTTAGGATGTTGGGAGCC 3942  
Db 3834 GAAGAGATCCGGATGATGGGTCACTCAACCATCAAAACATCATCCGGATGCTGGGGGCC 3893  
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Db 4014 TTACTCCGTGGCTTTCGTATCTCCATGAAGAACCAATCAATTCACAGAGATGTCAAAAGT 4073  
Qy 4123 GCCATTTGCTTAATATGAGGCTTCAAGAAATCAGTGTATTAATCACTACACTGACAG 4182  
Db 4074 GCCAATCTGCTCAATTCAGAGACCGGTTCAGAGGCTGAGAAATGTCAGACTTTTGGAGCTGT 4133  
Qy 4183 GCCAGGTGGCATCAAAAGGAACTGGTGCAGAGAGATTTTCAGGGACAAATTAATCGGGACA 4242  
Db 4134 GCCAGGTGGCATCAAAAGGAACTGGTGCAGAGAGATTTTCAGGGACAAATTAATCGGGACA 4193  
Qy 4243 ATTGCATTTATGGCACTGAGGTACTAAGAGGTCAACAGTATGGAAGAGCTGTGATGA 4302  
Db 4194 ATTGCATTTATGGCACTGAGGTACTAAGAGGTCAACAGTATGGAAGAGCTGTGATGA 4253  
Qy 4303 TGGAGTGTGGCTGTCTTATTAAGAAATGGCTTGTCAAAACCAACCATGGAATGCAGAA 4362  
Db 4254 TGGAGTGTGGCTGTCTTATTAAGAAATGGCTTGTCAAAACCAACCATGGAATGCAGAA 4313  
Qy 4363 AAACATCCATATCATCTTCTGTTGATATTAAGATGCTAGTGCACACTACTGCTCCATCG 4422  
Db 4314 AAACATCCATATCATCTTCTGTTGATATTAAGATGCTAGTGCACACTACTGCTCCATCG 4373  
Qy 4423 ATCCCTTCATCTTCTGTTTACAGATGCTGCTTCTGTTGTTAGAACTTCAA 4482  
Db 4374 ATCCCTTCATCTTCTGTTTACAGATGCTGCTTCTGTTGTTAGAACTTCAA 4433  
Qy 4483 CTTGAGGACAGACCTTCCATCAAGAGAGCTATGGAAGCATTCAGTCTTTCGTACTACATGG 4542  
Db 4434 CTTGAGGACAGACCTTCCATCAAGAGAGCTATGGAAGCATTCAGTCTTTCGTACTACATGG 4493  
Qy 4543 TAGCCAAATATGAGATCAACTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 4602  
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Qy 4603 TG----TGGGAAACCAATGATATTTCTACTGGCATGATGCTCACTGAACAGCTATGAAC 4658  
Db 4554 AGAACTTGTGGGCGACCATCGCGCTAAACCGCAGCCCTCACGCCACTGAACAGCCAGAAAC 4613  
Qy 4659 GAGGCGAGTGGGAAACCTTACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 4718  
Db 4614 GGGGCCAGCGGGGAA--CGTACTAGCATGTGTTGAAATATGATGATGATGATGATGATGATGATG 4672

Qy 4719 CTCAGTATGCA-AAAGCCCAAACTAGTGCAGAAACTGTAAACTGTGCTTTCAGAACT 4777  
Db 4673 CTCGATATGCGACATCTACAGCTGTGCAGAACTGCACACCGTGCCTTTCACAGGACT 4732  
Qy 4778 GCGCCCTAGTGTACAGGAAACATGAATTTGCTGATGATGATGATGATGATGATGATGATGAT 4837  
Db 4733 GCGCTCTGGGGACCGAGGAGCGATGGAGTTTGCATGACTAAAGAACAGAGCATAAAT 4792  
Qy 4838 TATTTTGGAGCACTTTTTCAGCAA 4864  
Db 4793 TA--TTTTGGAGCACTTTTTCAGCTA 4817

## RESULT 11

AAZ25072

ID AAZ25072 standard; cdNA; 5253 BP.

XX

AC AAZ25072;

XX

DT 09-DEC-1999 (first entry)

XX

DE Murine MEKK1 nucleotide sequence.

XX

KW MEKK1; MEKK2; MEKK3; mitogen-activated protein kinase; MAPK; ERK;

KW extracellular regulated kinase; signal transduction; regulation;

KW MAPK/ERK; MEK; MKKK; inflammation; cellular proliferation;

KW differentiation; development; cell death; ss.

XX

OS Mus musculus.

XX

FH Key

CDS Location/Qualifiers

FT 15..4496

FT /\*tag= a

FT /product= "MEKK1"

XX

PN WO9947686-A2.

XX

PD 23-SEP-1999.

XX

PF 15-MAR-1999; 99WO-US005556.

XX

PR 16-MAR-1998; 98US-0078153P.

PR

PR 04-SEP-1998; 98US-0099165P.

XX

PA (CADU-) CADUS PHARM CORP.

XX

PI Johnson GL;

XX

PI WPI; 1999-571843/48.

XX

DR P-PSDB; AAY42107.

XX

DR New human MEKK polynucleotides and polypeptides, used for regulating

XX

PT signal transduction in cells.

XX

PS Example 1; Fig 3; 159pp; English.

XX

CC The present sequence encodes murine mitogen-activated protein kinase/

CC extracellular responses kinase (MAPK/ERK) kinase kinase (MEKK),

CC specifically designated MEKK1. The MEKK proteins are used to modulate and

CC regulate signal transduction in cells, as well as for regulation of gene

CC transcription in a cell encoding MEKK, where the cell is involved in

CC inflammation, regulation of cellular proliferation and differentiation,

CC regulation of development, regulation of cell death or regulation of

CC inflammation. They are also used to prepare antibodies. MEKK

CC polynucleotides can be used to produce the protein recombinantly and as a

XX

SQ Source 5253 BP; 1299 A; 1403 C; 1433 G; 1118 T; 0 U; 0 Other;

XX

XX

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XX

XX

XX

XX

XX

XX

XX

XX

Query Match 65.1%; Score 3417; DB 2; Length 5253;  
Best Local Similarity 83.5%; Pred. No. 0;  
Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;

QY 1 GAGAAATGGCGGCGGCGGGAATCGCGCTCTGTCGCGGATTCGCGGCGCGCAGG 60  
Db 9 GAGAAATGGCGGCGGCGGCGGATCGCGCTCTGTCGCGGATTCGCGGCGCGCAGG 68  
QY 61 GCTACGAGCCTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 111  
Db 69 GCGCGAGTCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 128  
QY 112 GCGGCC--GCGGCTGCGCGGAGTCTGTCGCGGAGCGGCGGCGGCGGCGGCGGCGG 168  
Db 129 GCGGCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 188  
QY 169 GCGGACTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 228  
Db 189 GCGGACTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 248  
QY 229 GAGCAGCGGCTTCTTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 285  
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QY 286 GAGCCCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 345  
Db 309 GAGCCCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 368  
QY 346 CACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 405  
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QY 406 GCGGCTCGAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 465  
Db 429 GCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 458  
QY 466 TCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 525  
Db 459 CCCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 518  
QY 526 CACGAGTGTATGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 585  
Db 519 CACGAGTGTATGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 578  
QY 586 ATGCGAGCCTGGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 645  
Db 579 ATGCGGCTGGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 638  
QY 646 AAACCAATCCGAGTAAAGGAGATGATCTGAAATGAATCACTTAGCGCTGAGTCTCCA 705  
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QY 706 GGAGAGTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 765  
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Db 759 GCGAGCTCCGCTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 818  
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Db 1479 AAGTGGAGATCTCATGATTTCTACAGCCACAGATGTCAAGTCTGTGATTCCTCTCT 1538  
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Db 1599 AGGAATCAAGAGCAATTTTAACTTACTCATATGAACTTCACAAATCCCTCTCTCT 1658  
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QY 1843 AGCCCGAGTGGGGAGCCACAGTGGTCTTCCAGACAGTATCTCAGGAGATGTGTG 1902  
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QY 1903 GAGGATGTGCGAGCGCTTCTGTCAATGCTGTGTGCTGACCTCTCTACAAAGTGTACGTT 1962  
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QY 2083 GATGCAATAGCGGCAAGTGTGCTGATATCAACACTGTTGGAATGTGCAAGGC 2142  
Db 2079 GATGCAATAGCGGCAAGTGTGCTGATATCAACACTGTTGGAATGTGCAAGGC 2138  
QY 2143 CAGCAGGAGAGTGTGCGAGTGTGGCAGAAATTAATAAGCTGGATCCATTGGTATTGTT 2202

2139 CAAGCAGGAGCTGGCGGTTGGAGAGAAATACTTAAAGCTGGTCCATCGGGTTGCT 2198  
2203 GGTGTTGATTTATGTCCTTAATTTGATTTCTTGGAAACCAACTGATCAACAACTTGGCAA 2262  
2199 GGTGTGATTACGCTTTAAGTTGATCCCTTGGAAACCAAGCTGAATCAAAACAACTGGCAA 2258  
2263 GAACTTCTTGGCGCGCTTCTCTTATAGATAGACTGTTGTTGGAAATTCCTGCTGAATTT 2322  
2259 GAACTGCTGGTGGCTCTGCTTATAGACAGGTTGCTGTTGGAAATTCCTGCTGAATTC 2318  
2223 TATCCTCATATTTGTCAGTACTGATGTTTCAACAGCTGAGCCTGTTGAAATCAGGTATAAG 2382  
2319 TATCCTCATATTTGTCAGTACTGATGTTTCAACAGCTGAGCCTGTTGAAATCAGGTATAAG 2378  
2383 AAGCTGCTGCTCCCTTTAACTTTGCTTTGCAAGTCCATGATTAATCCCACTCAATGGTT 2442  
2379 AAGCTGCTCCTCCCTTTAACTTTGCTTTGCAATCCATGCAATTCCTCACTCGATGTT 2438  
2443 GGCAAACTTTCCAGAAAGATCTACTTGAGTTCTGCAAGATGTTTACTACAGTACCCCAT 2502  
2439 GGCAAGCTCTCTCGAGAGATATATCTGAGCTCTGCCAGGATGTTGACCCAGTGCCTGCT 2498  
2503 GTGTTTTCAAACTGTTAGAAATGCTGAGTGTTCAGATTTCCACTCACTTCCAGGATG 2562  
2499 GTGTTTTCAAGCTGGTAACTGCTTAAAGCTTCTGCTCCACCTTCCAGGATG 2558  
2563 CGTCGCGCTTGTGATTTGATTTGATGATGAGTGGAAATTCGCGAGCCATCCAGTTGGC 2622  
2559 CGCGGCTGCTGATGGCTTATCGCGGATGAGTAGAAATTCGCGAGTTCATCCAGCTGGT 2618  
2623 GTAGAAGACACTTTGGATGTTCAACAGAGCAGCTTCTTGAGGATCTGTTCCCAACAAC 2682  
2619 GTGAGGACACTGTGGATGGCATCAGGACAG----CTTACAGCGCTGGGCCCCCAGC 2675  
2683 TATCTGGAACCA CAGAGAACAGTTTCCCTGAGTGCAAGTCCATTTAGAGAACTGGA 2742  
2676 TGTCT-----AGAAAACAGCTCCCTTGAGCACACAGTCCATAGAGAGAACTGGA 2726  
2743 AAAGGATTTGCTTACAAAATTCAGTGCAGTTTCAGAGGACATTTCTGAGAGACTGGCC 2802  
2727 AAAGGACTAAGTGTACAGACTGAGTGCAGCTCGGAGGACATTTCTGACAGACTGGCC 2786  
2803 AGCAATTCAGTAGGACCTTCTAGTTTCAACAAACAAACAAACAAACAGAGAACCA 2862  
2787 GCGCTCTCTGAGGACTTCCAGCT-----CAACAAACAAACAGAACCA 2831  
2863 AAGCCAAATGTTTCAAAACAAAGGAGAGACCCACAGTCAAGTGTGAACTCTCTCCCTTA 2922  
2832 AAGCCAGCGGTTCAAAACAAAGGAGAGACCCACAGTCAAGTGTGAACTCTCTCCCTTTG 2891  
2923 TCTCATCATTTCCAAATTAATGTTTCCAGCCTTGTCAACCCCTTCTTCTTACCCCATCT 2982  
2892 TC---TCATGCTCAATTAATGTTTCCAGCACCATCAGCCCTTGTTCCTCTGCCCCGTCT 2948  
2983 GTACAGCTGGCACTGCAACAGATGTTCTAAGCATAGACTTCAGGATTCATTTCCCTGC 3042  
2949 GTCC-----CAGATTTCTAAGCACAGACCCAGGCAATTTGTTCCCTGCTG 2993  
3043 AGAATACCTTCTGCACTCTCTCAACACAGCGCAAGTTTCTCTACAAATTCACAGAAAC 3102  
2994 AAAATACCTTCCGATCTCTCAGACACAGCGCAAGTTCTCTCTACAAATTCACAGGAAC 3053  
3103 TGTCTGAAAACAAAGACTCAGATAAATTTCCCGAGTCTTACTCAGTCAAGACCTTGG 3162  
3054 TGTCTGAAACACCGAGACTCAGACCAAGTCTCTCCAGTCTTCACTCAGTCAAGACCCCA 3113  
3163 CCTCCAGTAAACATACAGAGGCAAGGCACTAGACCTACCCAGGTAATACAAAGTAAA 3222  
3114 CCTCCAGTAAACATACAGAGGCAAGGCACTCCCGAGTCTCCGGGCAAGTAAAGCAA 3173  
3223 CAGGGAGATCCCTCAAAAATAGCATGACATTTGATCTGAACAGTAGTTTCAAAATGAT 3282

3174 CTAGGGACGCCAACAAAAGTAGCATGACACTTGAATCTGGCAGTGTCTCCAGGTGTGAC 3233  
3283 GACAGCTTTGGCTCTAGCAGCAATAGTAGTAATGCTGTATATCCAGTGAACGACAGTGT 3342  
3234 GACAGCTTTGGCGCGCGGCAACAGTGGCAACGCGCTCATATCCACGACGACGACAGTGT 3293  
3343 TTCAACCCAGTAGAGGAGAAATGACAGATTAGATGTCAATACAGAGCTCAATCCAGTATT 3402  
3294 TTCACGCGGTGGAGGCAAGTGCAGGTTAGATGTGAACACCGAGCTCAATCCAGGATC 3353  
3403 GAGGACCTTCTTGAAGCATCTATGCTTCAAGTGATACAAACAGTAACTTTTAACTCAGAA 3462  
3354 GAGGACCTTCTTGAAGCATCTATGCTTCAAGTGACACGACAGTCACTTTCAAGTCCGAA 3413  
3463 GTTCGTCCTGCTCTCTGAAAAGGCTGAAATGATGATACCTTACAAAGATGATGTGAAT 3522  
3414 GTGCGCTGCTCTCTCTCGGAAAAGCGGCAAAATACGACACCTTACAAAGACGAGCTCAAT 3473  
3523 CATTAATCAAAAGTGCAAAGACAGATGGAAGCTCAAGAAAGAAAGCTTTAGCAATTTGCC 3582  
3474 CATTAATCAAAAGTGCAAAGAAAGATGGAAGCTGAAGGAGGAGGCTTTAGCGATGCC 3533  
3583 ATGCAATGTGAGGCTCTCAGGATGCCCTCCCATAGTTCTCTCAGCTGCGAGTTGAAAT 3642  
3534 ATGCGATGTGAGGCTCTCAGGATGCCCTCCCATAGTTCTCTCAGCTGCGAGTTGAAAT 3593  
3643 GGAGAGATATCATCATTTTCAACAGGATACACAGAGACTCTACAGGACATACCAA 3702  
3594 GGAGAGATATTTATCATTTTCAAGGACACACAGAACTCTTCCAGGACATACCAA 3653  
3703 GCAAAACACCGTATAGAGAGACACATGATGGCTGAAAGTCAACAGATAGGCTTGGGA 3762  
3654 GCAAAACACCGCTTACAGAGAGACCGCTGAGTGGCTGAAAGGCCAGAGATAGGCTTCGGA 3713  
3763 GCATTTCTTCTGTTATCAGGCTCAAGATCTGGGAACTGGAATTTTAAATGGCTGTTAAA 3822  
3714 GCATTTCTTCTGTTATCAGAGCAGAGATGTGGGACTGGGACTTTTAAATGGCTGTGAA 3773  
3823 CAGGTGACTTATGTGAGAAACACATCTTCTGAGCAAGAAAGTAGTAGAGACTAAGA 3882  
3774 CAGGTGACTTATGTGAGAAACACATCTTCCGAGCAGGAGAGGTTGGTGGAAAGCTTTGAGG 3833  
3883 GAAGAGTAAAGTATGATGAGCCTGATCATCAAAACATCATTTAGGATGTGGGAGCC 3942  
3834 GAAGAGTCCGGATGATGGTCACTCAACCATTCCAAACATCTCCGAGATGTCTGGGAGCC 3893  
3943 ACGTGTGAGAGAGCAATTTACAAATCTTCTTGAATGGATGGCAGGAGGATCGGTGGCT 4002  
3894 ACGTGTGAGAGAGCAATTTACAACTCTTCTTGAATGGATGGCAGGAGGATCTGTGGCT 3953  
4003 CATTTGCTGAGTAAATATGGAGCCTTCAAGAACTAGTAGTTATTAATACACTGAAACAG 4062  
3954 CACCTCTTGAATTAATACGAGCTTTCAAGGAGTCACTCGTCAATTAATCACTGAGCAG 4013  
4063 TTACTCCGTGGCTTTCTGATCTCCATGAAAACCAAAATCATTTCAGAGATGTCAAAGT 4122  
4014 TTACTCCGTGGCTTTCTGATCTCCATGAAAACCAAAATCATTTCAGAGAGCTCAAAGT 4073  
4123 GCCAATTTGCTTAAATGACAGCACTGTCAGAGACTTAAGAAATGACAGATTTGGGCTGCA 4182  
4074 GCCAATTTGCTTAAATGACAGCACTGTCAGAGCTTCAAGGAGTCACTCGTCAATTAATCACTGAGCTGT 4133  
4183 GCCAGGTTGGCATCAAAAGGAACTGTCAGAGAGTTCAGGGGCAAAATTTACTGGGGACA 4242  
4134 GCCAGGTTGGCATCAAAAGGAACTGTCAGAGAGTTCAGGGGCAAGTTCAGGGGACA 4193  
4243 ATTGCAATTTATGGCACTGAGGATTAAGAGTCAACAGTATGGAAGGAGCTGTGATGA 4302  
4194 ATTGCAATTTATGGCACTGAGGATTAAGAGTCAACAGTATGGAAGGAGCTGTGATGA 4253  
4303 TCGAGGTTGGCTGTGCTTATTAAGAAATGGCTTGTGCAAAACCAACCACTGGAAATCAGAA 4362  
4254 TCGAGGTTGGCTGTGCTTATTAAGAAATGGCTTGTGCAAAACCAACCTTGGAAATCAGAA 4313

QY 4363 AAACACTCCAATCATCTTGTCTTTGATATTTAAGATTGCTAGTGCACAACTACTGTCTCCATCG 4422  
 DB 4314 AAACACTCCAATCATCTTGTCTTTGATATTTAAGATTGCTAGTGCACAACTACTGTCCATCG 4373  
 QY 4423 ATCCCTTACATTTGTCTCTGTTTACGAGATGCTGCTTCTTTAGAACTTCAA 4482  
 DB 4374 ATCCCGTCACACCTGTCTCCCGGCTCTGCGACGCTGCGCTCTTGTAGAACTTCAG 4433  
 QY 4483 CCTCAGGACAGACCTCCATCAAGAGAGCTACTGAAGCATCCAGTCTTCTGTAATGAG 4542  
 DB 4434 CCTCAGGACCGCTCTCGTCAGAGAGCTGCTGAACATCCGCTTCTGTAACAGCTGG 4493  
 QY 4543 TAGCCAAATATGAGATCAACTACAGTAGAAACAGGATGCTCAACAGAGAGAAAAA 4602  
 DB 4494 TAGTTAATTTGATCAGCTCAATGAGACAGGATATGCAACCGGAGAGAGAAAG 4553  
 QY 4603 TG---TGGGGAACACATTTGATATTTCTACTGGCCATGATGCCACTGAACAGCTATGAAC 4658  
 DB 4554 AGAACTTGTGGGACCAATGCGCTAACCGCAGCCCTCACGCCACTGAACAGCCAGAAC 4613  
 QY 4659 GAGGCCAGTGGGGAACCCCTTACCTAAGTATGTGATTGACAAATCATGATCTGTACCTAAG 4718  
 DB 4614 GGGGCCAGCGGGAA-CGGTACCTAAGCATGTGATTGACAAATCATGACCTGTACCTAAG 4672  
 QY 4719 CTCAGTATGCA-AAAGCCCAACTAGTGCAGAACTGTAACTGTGCTTTCAAGAACT 4777  
 DB 4673 CTCGATATGACAGATCTTACAGCTCGTGCAAGAACTGCACACCGTGTCTTACAGGACT 4732  
 QY 4778 GGCCTTAGTGAACAGAGAAAACAATGAAGTTTGCATGACTAAATTTGAGAAAGCATATTT 4837  
 DB 4733 GGCTCTGGGGACCAAGGCGATGGAGTTTGCATGACTAAAGAAACAGAGCATATAAT 4792  
 QY 4838 TATTTTGTGAGCACTTTTTCAGCAA 4864  
 DB 4793 TA--TTTGTGAGCACTTTTTCAGCTA 4817

## RESULT 12

AD44414  
 ID AD44414 standard; DNA; 5253 BP.

XX AC AD44414;

XX DT 13-DEC-2002 (first entry)

XX DE Mouse MEK1 DNA.

XX KW Mitogen-activated protein kinase; MAPK; MAPK kinase; MEK; MEK kinase 1;  
 MEK1; apoptosis; caspase protease; anti-apoptotic; autoimmune disease;  
 allergic reaction; inflammation; neurological disorder; cancer;  
 hormone-related disease; apoptotic; cytostatic; immunosuppressive;  
 antiinflammatory; nootropic; neuroprotective; endocrine-gen; mouse;  
 enzyme; gene; ds.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

XX FT CDS 15..4496

XX FT /tag= a

XX FT /product= "Mouse MEK1"

XX PN US2002055130-A1.

XX PD 09-MAY-2002.

XX PF 16-MAY-2001; 2001US-00858754.

XX PR 14-FEB-1997; 97US-0039740P.

XX PR 13-FEB-1998; 98US-00023130.

XX PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

PI Johnson GL;

XX WPI: 2002-462905/49.

XX P-PSDB; AAE26657.

XX New isolated protease resistant mitogen-activated protein kinase kinase  
 PT kinase protein used for inhibiting apoptosis and treating diseases, such  
 PT as, cancer, autoimmune diseases, allergic reactions, and inflammation.

XX Disclosure; Page 68-73; 97pp; English.

XX The invention relates to protease-resistant mitogen-activated protein  
 CC kinase (MAPK) kinase (MEK) kinase 1 protein, designated MEK1 and its  
 CC corresponding nucleic acid. MEK1 is used to inhibit apoptosis. MEK1  
 CC fragment is used to stimulate apoptosis. The fragment is used to identify  
 CC a compound that modulates the apoptotic activity of the fragment. MEK1  
 CC is used to identify a compound that modulates the proteolytic cleavage of  
 CC the protein by a caspase protease is used to treat diseases such as  
 CC cancer, autoimmune diseases, allergic reactions, inflammation,  
 CC neurological disorders, or hormone-related diseases. The present sequence  
 CC is mouse MEK1 DNA

XX Sequence 5253 BP; 1299 A; 1403 C; 1433 G; 1118 T; 0 U; 0 Other;

XX Query Match 65.1%; Score 3417; DB 6; Length 5253;

XX Best Local Similarity 83.5%; Pred. No. 0;

XX Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;

QY 1 GAGAAATGGCGCGCGCGCGGGAATCGCGCTCTGTCGTCGGGATCCCGGCGCCAGG 60

DB 9 GAGAAATGGCGCGCGCGCGGCGATCGCGCTCTGTCGTCGGGATCCCGGCGCCAGG 68

QY 61 GCTAGAGCCCTGAGCGAGCGCGCGCGC-----GGAGGAGCCCTCAAGCGAGCAGC 111

DB 69 GCGCGAGTCCCGAGCGCGCGCGCGCGCGCGAGGAGGAGGAGCTCTCAGGAGAGCGGC 128

QY 112 GCGCCC---GCGGCTGCGCGGAGCTGTGCGGAGGCGGCGAGCGGGGCGCGAGCGG 168

DB 129 GCGCGCGAGCGCGCGCGCGCGCGCTGTGCGGAGCTGTGCGGCGCGCGCGCGAGCGC 188

QY 169 GCGGACTGCGCGCGCGCGCGAGCTGCGCAAGTGTGCGGAGTGTGAGCTGGACCGAGTGCCT 228

DB 189 GCGGACTGCGCGCGCGCGCGAGCTGTGCGCAAGTGTGCGGAGTGTGAGCTGGACCGAGTGCCT 248

QY 229 GAGCAGCGCTCTTCTTCTGCGCGCTCACCGCGCGCT---CCTGACTTCCCGTGC 285

DB 249 GAGCAGCGCTCTTCTTCTGCGCGCTCACCGCGCGCTCACCTTCTTCTTCTTCTTCTTCTTCT 308

QY 286 GAGCGCGCGAGCGAGCGCGGAGTGGGACCGGCTTCCAGCTGTGCGGTGCGCGCGCG 345

DB 309 GAGCGCGCGAGCGCGGCTCGAGAGCGAGTGTGCTTCCAGCGCGCGCGGAGCGCGCACCC 368

QY 346 CACGAGCGCGAGCG 405

DB 369 CCGGAGCGCGAGTGTGCTGCGCTTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 428

QY 406 GCGGCTTCTGAGTCCCGAGCG 465

DB 429 GCGCGCGCGAGCG 458

QY 466 TCTCTTCTGAGCG 525

DB 459 CCTCTTCTGAGCG 518

QY 526 CACAAGAT 585

DB 519 CACAAGAT 578

QY 586 ATGCCAGCTGGAAGCAGCAATGTTGGAAGAGAGAAATAGCGAGGCGCGCTGTGTGTGTA 645

DB 579 ATGCCAGCTGGAAGCAGCAATGTTGGAAGAGAGAAATAGCGAGGCGCGCTGTGTGTGTA 638

QY 646 AAACCAATCCAGTTAAAGAGATGATCTGAATGAATCACTTAGCAGCTGAGTCTCCA 705

639	1719	TTCTCTAGAAA	CTGGAACGTAAGG	AAATGGCCCTTAGCGCTCTTTCCCA	CGACGTTAGT	1778	
1783	1783	GGGGCCCTGCTGT	TGGCAAAATGGG	AGAGCACTGGA	AAATTCGCGGGG	CAGACAGTGGAAAGC	1842
1779	1779	GGGGCCCTGCTGT	TGGCAAAATGGG	AGAGCACTGGA	AAATTCGCGGGG	CAGACAGTGGGGGC	1838
1843	1843	AGCCGAGTGGGG	AGCCACCACTG	TGGGTCTTCC	CAGACCAAGTATCT	CAGGAGATGTGGTG	1902
1839	1839	AGCTTAAGCGGG	AGCGGCGGCTCT	CCAGCC	CAGCATCTC	CAGGSGATCTGGTG	1898
1903	1903	GAGCATGCTGAG	CGTTCTGTCAAT	AGTGTGTGTG	TGACCCCTGTCT	CAAAAGTGTACGTT	1962
1899	1899	GAGCGTCTGCA	GTGTCTGTATAGT	CTCGTGAC	CCCTGTCTT	ACAAAGTGTACGTT	1958
1963	1963	GCTCTTTAAAAA	CATTGAGAGC	ATGCTGTATAC	TCTTCTG	CGCAAGTTTACGGAA	2022
1959	1959	GCTCTTTAAAAA	CATTGAGAGC	ATGCTGTATAC	TCTTCTG	CGCAAGTTTACGGAA	2018
2023	2023	AGAAATCAAACT	TTCAGAGACTT	CTCCAGC	AGTTGTAGAC	CACTCTAGTCAAAATGTGCA	2082
2019	2019	AGAAATCAAACT	TTCAGAGACTT	CTCCAGC	AGTTGTAGAC	CACTCTAGTCAAAATGTGCA	2078
2083	2083	GATGCCAATAGC	CGCACAGT	CTGCTCATAT	CAACACTGT	TGGAATGTGCAAAAGC	2142
2079	2079	GATGCCAAGCG	CGCACAGT	CTGCTCATAT	CAACACTGT	TGGAATGTGCAAAAGC	2138
2143	2143	CAAGCAGAGAGT	TGGCAGT	TGGCAGAGAAAT	CTCTAAAAGCT	TGGATTCGATTTGGT	2202
2139	2139	CAAGCAGAGAGT	TGGCAGT	TGGCAGAGAAAT	CTCTAAAAGCT	TGGATTCGATTTGGT	2198
2203	2203	GGTGTGATTAT	GTCTTTAAAT	TGTATTCTT	TGGAACCAAACT	GAATCAAAATTTGGCAA	2262
2199	2199	GGTGTGATTAT	GTCTTTAAAT	TGTATTCTT	TGGAACCAAACT	GAATCAAAATTTGGCAA	2258
2263	2263	GAACTTCTTGG	CGCCTTGTCTT	ATAGATAGACT	CTGTTGGAATTT	CTCTGCTGAATTT	2322
2259	2259	GAACTTCTTGG	CGCCTTGTCTT	ATAGATAGACT	CTGTTGGAATTT	CTCTGCTGAATTT	2318
2323	2323	TATCCTCATAT	TGTCACTAGT	TTTCAAGCT	CGACCTGTT	GAAATCAAGGTATAAG	2382
2319	2319	TATCCTCATAT	TGTCACTAGT	TTTCAAGCT	CGACCTGTT	GAAATCAAGGTATAAG	2378
2383	2383	AGCTGCTGCTCC	CTTTAAACCTT	TGCTTTCAGT	CTCATTGATAT	TTCCCACTCAATGGTT	2442
2379	2379	AGCTGCTGCTCC	CTTTAAACCTT	TGCTTTCAGT	CTCATTGATAT	TTCCCACTCAATGGTT	2438
2443	2443	GGCAAACTTTC	CAGAAGGATCT	ACTCGATTCT	CGAAGATGTT	ACTCAGTACCCCAT	2502
2439	2439	GGCAAACTTTC	CAGAAGGATCT	ACTCGATTCT	CGAAGATGTT	ACTCAGTACCCCAT	2498
2503	2503	GTGTTTTCAAA	AACTGTTAGAA	ATGCTCAGT	TTTCCAGTTC	CACTTCCACGAGATG	2562
2499	2499	GTGTTTTCAAA	AACTGTTAGAA	ATGCTCAGT	TTTCCAGTTC	CACTTCCACGAGATG	2558
2563	2563	CGTCCCGCTTT	GATGGCTATT	TGCAGATG	AGGTGGAAAT	TCGGAAGCATCTCAGTTGGGC	2622
2559	2559	CGTCCCGCTTT	GATGGCTATT	TGCAGATG	AGGTGGAAAT	TCGGAAGCATCTCAGTTGGGC	2618
2623	2623	GTAGAGACACT	TTTGGATGGT	CAACAGAG	CAGCTTTCTT	CGAGCATCTGTTCCCAACAAC	2682
2619	2619	GTAGAGACACT	TTTGGATGGT	CAACAGAG	CAGCTTTCTT	CGAGCATCTGTTCCCAACAAC	2675
2683	2683	TATCTGGAAA	CCACAGAGAA	CAGTTCCCT	TGAGTGAC	AGTCTCATTTAGAGAAAATCTGGA	2742
2676	2676	TGCTCT-----	AGAAAA	CAGCTCCCT	TTGAGCAC	CAGTCTCATAGAGAAAATCTGGA	2726
2743	2743	AAAGGATTAT	TGTCTACAAA	ATTCAGT	TGCGCAGT	TTCTGAGAGACATTTCTGAGAGACTGGCC	2802
2727	2727	AAAGGATTAT	TGTCTACAAA	ATTCAGT	TGCGCAGT	TTCTGAGAGACATTTCTGAGAGACTGGCC	2786
2803	2803	AGCATTTCA	TGATGACCTT	CTTAGTTT	CAACAACA	CAACAACAAGAGACCA	2862
2787	2787	GGCGTCTCT	GTAGACTTCC	CAGCT-----	CAACAACA	CAACAACAAGAGACCA	2831

QY 2863 AAGCAATGGTTCAAAACAAAGGAGAGACCCACAGTCAGTGTGTTGAACTCCTCTCCCTTTA 2922  
DB 2832 AAGCAGCGGTTCAAAACAAAGGAGAGACCCACAGTCAGTGTGTTGAACTCCTCCCTTTG 2891  
QY 2923 TCTCATCTTCCCAATTAATGTTTCCAGCCTGTGCAACCCCTTCTTCTTCTACCCCATCT 2982  
DB 2892 TC---TCATGCTCAATTAATGTTTCCAGCAGCACCATCAGCCCTTGTCTCTGCCCCGCT 2948  
QY 2983 GTACAGCTGGCAGCTGCAACAGATGTCTTAAGCATAGACTTTCAGGGATTTCATTCCTGSC 3042  
DB 2949 GTCC-----CAGATATTTCTAAGCAGACCCAGGCAATTTGTTCCCTGSC 2993  
QY 3043 AGAATACCTTCTGATCTCCTCAACACAGCGCAAGTGTCTTCTACAAATTCACAGAAAC 3102  
DB 2994 AAAATACCTTCCGCACTCCTCAGACACAGCGCAAGTGTCTTCTACAAATTCAGAGGAAC 3053  
QY 3103 TGTCTCTGAAACAAAGACTCAGATAAATTTCCCAAGTCTTTTACTCAGTCAAGACCCCTTG 3162  
DB 3054 TGCTCTGAACACCGAGACTCAGACAGCTCTCCAGAGTCTTCCAGTCAAGACCCCA 3113  
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QY 3223 CAGGGAGATCCCTCAAAAATAGCATGACACTTGTATGTAACAGTAGTTTCCAAATGTGAT 3282  
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QY 3283 GACAGCTTTGGTGTAGAGCAATAGTAGTAATGTGTTATACCCAGTGAAGAGACAGTG 3342  
DB 3234 GACAGCTTTGGCGCGCGGCAACAGTGGCAACCGCGTCTATACCCAGCGACGAGACAGTG 3293  
QY 3343 TTCACCCAGTAGAGAGAAATGCAATAGATGTCAATACAGAGCTCAACTCCAGTATT 3402  
DB 3294 TTCGCGCGGTGAGAGCAAGTGCAGTTAGTGTGAACACCGAGTCAACTCCAGCATC 3353  
QY 3403 GAGGACCTTCTGAAGCATCTATGCTTCAAGTGTATACAAACAGTAACTTTTAAGTCAGAA 3462  
DB 3354 GAGGACCTTCTGAAGCATCTATGCTTCAAGTGTATACAAACAGTCACTTTCAAGTCGAA 3413  
QY 3463 GTTGTCTCTGCTCTCTGAAGAGGTGAATGTATGATGTACCTACAAAGCATGTGAT 3522  
DB 3414 GTGCGCGTCTCTCTCCGGAAGAGGCGGAAATGACGACCTTACAAAGACGAGTCAAT 3473  
QY 3523 CATAATCAAAAGTCAAGAGAGATGGAAGCTGGAAGAGAGAGAGCTTTAGCAATTTGCC 3582  
DB 3474 CATATCAAAAGTCAAGAGAAAGATGGAAGCTGGAAGAGAGAGGAGGCTTTAGCGATGCC 3533  
QY 3583 ATGGCAATGTACAGGTCTAGGATGCGCTCCCATAGTTCCTCAGCTGCAAGTTGAAAT 3642  
DB 3534 ATGGCGATGTACAGGTCTCAGGATGCGCTCCCATAGTTCCTCAGCTGCAAGTTGAAAT 3593  
QY 3643 GGAGAGATATCATCATTTCAACAGGATACACAGAGACTCTACAGGACATACCAAA 3702  
DB 3594 GGAGAGATATATCATCTTACAGGAGACACACAGAGAACTCTTCCAGGACATACCAAA 3653  
QY 3703 GCAAAACACCGTATAGAGAGACACATGAATGCTGAAAGTCAACAGATAGCGCTTGA 3762  
DB 3654 GCGAAACAGGCTTACAGAGAGACGCTGAGTGTGCTGAAAGGCGCAGAGATAGCGCTCGGA 3713  
QY 3763 GCATTTCTTCTTGTATCAGGTCAAGATGTGGGAACCTGGAATTTAATGGCTGTAAA 3822  
DB 3714 GCATTTCTTCTTGTATCAGGACACAGGATGTGGGACTGGGACTTTAATGGCTGTAAA 3773  
QY 3823 CAGTGACTTATGTACAGAAACATCTTCTTGAGAGAGAGAGAGATAGTAGAGCACTAAGA 3882  
DB 3774 CAGTGACGTACGTACAGAAACATCTCCTCCAGCAGGAGGAGGTGTGGAAGCGTTGAG 3833  
QY 3883 GAGAGATAGATAGTACGCACTCTCAATCAATCCCAACATCATTAGGATGTTGGGAGCC 3942  
DB 3834 GAAGAGATCCGATGATGGGTACCTCAACCATCCCAACATCATCCGGATGCTGGGGGCC 3893

QY 3943 ACCTGTGAGAGAGCAATTAACAATCTCTTCAATTGAATGGATGGCAGGGGATCGGTGGCT 4002  
DB 3894 ACCTGTGAGAGAGCAATTAACAATCTCTTCAATTGAATGGATGGCAGGGGATCGGTGGCT 3953  
QY 4003 CATTTGCTGAGTAAATATAGGAGCTTTCAAGAAATCAGTAGTATTATTAACTACACTGAACAG 4062  
DB 3954 CACTCTTGTAGTAAATACGAGGCTTTCAAGAGTCACTGCTCATTAACACTACACTGAGCAG 4013  
QY 4063 TTACTCGGTGGCTTCTGCTATCTCCATGAAACCAAAATCAATTCACAGAGATGTCAGAGT 4122  
DB 4014 TTACTCGGTGGCTTCTTCTATCTCCAGAGAACAGATCATTCACAGAGACGTCAGAGGT 4073  
QY 4123 GCCAATTTGCTAATTCAGACGACTGTGTCAGAGACTAAGAAATTCAGATTTTGGAGCTGCA 4182  
DB 4074 GCCAATCTGCTCATTCAGACGACCGGTTCAGAGCTGAGATTCAGACCTTTGGAGCTGCT 4133  
QY 4183 GCCAGGTTGGCATCAAAAGAACTGTGTGAGAGAGTTCAGGGAACAATTAATCTGGGGACA 4242  
DB 4134 GCCAGGTTGGCATCAAAAGAACTGTGTGAGAGAGTTCAGGGAACAATTAATCTGGGGACA 4193  
QY 4243 ATTGCAATTTATGCACTGAGGTACTAAGAGGTCAACAGTATGTAAGAGGAGCTGTGATGTA 4302  
DB 4194 ATTGCAATTTATGCGGCTGAGGTCTTAAGAGGTTCAGAGTATGTAAGAGGCTGTGATGTA 4253  
QY 4303 TGGAGTGTGGCTGTGCTATTATAGAAATGGTGTGCAAAACCAACCATGGAATGCAAGAA 4362  
DB 4254 TGGAGTGTGGCTGTGGCTATTATAGAAATGGTGTGCAAAACCAACCATGGAATGCAAGAA 4313  
QY 4363 AAACACTCCCAATCATCTTGTGATATTAAGATGCTAGTCAACTACTGCTCCATCG 4422  
DB 4314 AAACACTCCCAATCATCTTGTGATATTAAGATGCTAGTCAACTACTGCTCCATCG 4373  
QY 4423 ATCCCTTCAATTTGTCTCTGCTTACGAGATGTGCTCTTCTGTTGTTTGAACCTTCAA 4482  
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QY 4483 CCTCAGACAGACCTCCATCAAGAGAGCTACTGAGCATCCAGTCTTTCGTACTTACATGG 4542  
DB 4434 CCTCAGACAGCGGCTCCGTCAGAGAGCTGTGAAACATCCGGTCTTCCGTACCACTGG 4493  
QY 4543 TAGCCAATTTAGCAGATCAACTACAGTAGAAACAGGATGTCTCAACAGAGAGAAACAACT 4602  
DB 4494 TAGTTAATTTGTCAGATCAGCTCTAATGGAGACAGGATATGCAACCGGAGAGAGAAAG 4553  
QY 4603 TG----TGGGAAACCAATTGATATTCTTCTGCGCATGATGCCACTGAAACAGCTATGAAC 4658  
DB 4554 AGAACTTTGTGGCGACCATGCCGCTAACCGCAGCCCTCACGCCACTGAAACAGCGCAAC 4613  
QY 4659 GAGGCGAGTGGGAAACCTTTACCTAAGTATGTGATTCACAAATCATGATCTGTACCTTAAG 4718  
DB 4614 GGGGCGAGCGGGAA--CGTACCTAAGCATGTGATTCACAAATCATGATGATGATGATGAT 4672  
QY 4719 CTCAGTATGCA--AAAGCCCAAACTAGTGCAGAACTGTAAACTGTGCTTTCAGAGAACT 4777  
DB 4673 CTCGATATGCAAGACATCTACAGCTCGTGCAGAACTGCAACCGTGTCTTTCAGAGACT 4732  
QY 4778 GGCCCTAGTGAACAGAGAAACATGAAGTTTGCATCACTAAATTTGAGAGAGCAATATTT 4837  
DB 4733 GGCTGTGGGACCCAGAGAGCGGATGAGTTTGCATGATTAAGAAACAGAGCAATATTT 4792  
QY 4838 TATTTTGTGAGCACTTTTTCAGCAA 4864  
DB 4793 TA--TTTTTGGAGCACTTTTTCAGCTA 4817

RESULT 13

AAL41578

ID AAL41578 standard; cDNA; 5539 BP.

XX

AC AAL41578;

XX

DT 19-APR-2002 (first entry)

XX





Db 1646 AGAGCCTGACTGTGTGAAGATGGCTGCGAGAAACAGCTGCAACCACTTGATGTCCA 1705  
Qy 1427 TTTGGGAGAGAGTGTAGAAGAAATAGAGAACCTTTAATATGTGTCCTTTGTAGATCTA 1486  
Db 1706 TCTGGCGGAGAGTGTAGAAGAAATAGAGAGCCTTTAATATGTGTCCTTTGTAGATCTA 1765  
Qy 1487 AGTGGAGATCTCATGATTTCTACAGCCACAGTGTCAAGTCTGTGGATCCCTTCCTT 1546  
Db 1766 AGTGGAGATCCCATGATCTTCTACAGCCATGAGTTATCAAGCCCGTGGATCCCGCCCT 1825  
Qy 1547 CCCTCAGAGTGCACAGCAGCAACCGTACAGCAGCAGCCTTTGGCTGGATCA---CGAA 1603  
Db 1826 CCCTGCGAGTGTCCAGCAGCCATCTCTCCCGCAGCAGCCGTTGGCCGATCACAGCGA 1885  
Qy 1604 GGAATCAAGAGAGCAATTTTAACTTACTCATATGAACTCAGCAATCCCTCCGCTT 1663  
Db 1886 GGAATCAGGAGAGCAGTTTAACTTACTCATATTTGAAACCCAGCAGATTTCTTCGCTT 1945  
Qy 1664 ACAAAGATTTAGCTGAGCCATGGATTCAGGTGTTTGAATGGAACTCGTTGGCTGCTTAT 1723  
Db 1946 ACAAGATTTGGCCGAGCCATGGATTCAGGTGTTTGAATGGAACTCGTTGGCTGCTTAT 2005  
Qy 1724 TTTCTAGAACTGGAATGTAGAGAGATGGCCCTCAGCGCTCTTCCCATGATGTCAAGT 1783  
Db 2006 TCTCTAGAACTGGAACGTAAAGGAAATGGCCCTTAGCGCTTTTCCCAACGACGTTAGTG 2065  
Qy 1784 GGGCCCTCTGTGGCAATGGGAGAGCACTGGAATTTCTGGGGCAGCAGTGGAGCA 1843  
Db 2066 GGGCCCTGTGTGGCAACGGGAGAGCACTGGAATTTCTGGAGCGGCGAGTGGGGCA 2125  
Qy 1844 GCGGAGTGGGGAGCCACAGTGGGTCTCCAGACAGTATCTCAGGAGATGTGTGG 1903  
Db 2126 GCTTAAAGCGGGAGCGCCAGCGGTCTCCAGCCAGCATCTCAGGGGATGTGTGG 2185  
Qy 1904 AGGCATGCTCAGAGTCTGTCAATGTTGCTGTGACCTGTCTACAAAGTGTACGTTG 1963  
Db 2186 AGGCGTGTGAGTGTCTGTCTATAGTCTGCTGACCTGTCTCAAAAGTGTACGTTG 2245  
Qy 1964 CTGCTTTAAACATTTAGAGCCATGTGTGTATATCTTCTGTCACAGTTTAGCGGAAA 2023  
Db 2246 CTGCTTTAAACATTTAGAGCCATGTGTGTATACACTCTCTTGCACAGTGTGCGAGAA 2305  
Qy 2024 GAATCAAACTTCAGAGCTTCTCAGCCAGTGTAGACACCATCTAGTCAAAATGTGCGAG 2083  
Db 2306 GAATCAAACTTCAGAGCTCTCTCGGCGAGTGTAGACACTATCTTGTCAAGTGTGCGAG 2365  
Qy 2084 ATGCCAATAGCCGACAAAGTCAGTGTCTCATATCAACACTGTGTGAACTGTGCAAGGCC 2143  
Db 2366 ATGCCAACAGCGCACGAGTCAGCTGTCCATATCTACAGTCTGGAACCTGTGCAAGGCC 2425  
Qy 2144 AAGCAGGAGTGTGCGAGTGTGCGAGAGAAATCTAAAGCTGGATCCATTTGGTATGGTG 2203  
Db 2426 AAGCAGGAGTGTGCGGTTGGGAGAGAAATCTTAAAGCTGGGTGCCATGGGGTTGGTG 2485  
Qy 2204 GTGTTGATTTATCTTAAATTTGATTTCTTGAACCAAACTGAAATCAAACTTTGGCAAG 2263  
Db 2486 GTGTCGATTAAGTCTTAAGTTGTATCTTGGAAACCAAGCTGAATCAAACTTTGGCAAG 2545  
Qy 2264 AACTTCTTGGCGCCTTTGTCTTATAGATAGACTGTTTGGAAATTTCTGCTGAAATTT 2323  
Db 2546 AACTGCTGGGTGCGCCTGTCTTATAGACAGTTGCTGTGGAAATTTCTGCTGAAATTT 2605  
Qy 2324 ATCCCTCATATTTCTCAGTACTGATGTTTCAAGCTGAGCCTGTGAAATCAGGTATAGA 2383  
Db 2606 ATCCCTCATATTTCTCAGTACTGATGTTTCAAGCTGAGCCTGTGAAATCAGGTATAGA 2665  
Qy 2384 AGCTGCTGCTCTTAACTTTGCTTTGCGAGTCAATGATTAATTTCCCACTCAATGGTTG 2443  
Db 2666 AGCTGCTCTCTTAACTTTGCTTTGCGATCCATTTGCAATTTGCAATTTCCCACTCGATGGTTG 2725  
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Db 2726 GCAAGCTCTCTCGGAGGATATATCTGAGCTCTGCCAGGATGGTGACGCGAGTGCCTCGCTG 2785  
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Qy 2564 GTGCGCGTGTGATGGCTATTGTCAGATGAGTGGAAATTTGCCAGGATCCAGTGTGGCG 2623  
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Db 2963 GTCT-----AGAAAACAGCTCCCTTGAGCACACAGTCCATAGAGAAAACCTGAA 3013  
Qy 2744 AAGGATTTAGTCTCAAAATGAGTGCAGTTCAGAGGACATTTCTGAGAGACTGGCA 2803  
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Qy 3104 GTCTGAAACAAAGACTCAGATAAACTTTCCCACTCTTTACTCAGTCAAGACCTTGC 3163  
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Db 3401 CTTCTAGTAACTATACAGGCGCAAGCCATCCCGACCCGTTCCGGGCGAGTACAGCAAC 3460  
Qy 3224 AGGAGATCCCTCAAAATTAGCATGACACTTTGATCTGAACAGTAGTTCCTCAATGTGATG 3283  
Db 3461 TAGGGACCGCACAAAAGTAGCATGACACTTTGATCTGGGCACTGCTTCCAGTGTGAG 3520  
Qy 3284 ACAGCTTTGGCTGTAGCAATATAGTAATGCTGTGTTATACCCAGTACAGACAGTGT 3343  
Db 3521 ACAGCTTTGGCGCGCGGCAACAGTGGCAACCGCTCTATACCCAGCGACAGAGTGT 3580  
Qy 3344 TCACCCCTGTAGAGGAGAAATGACAGATTAGATGTCAATACAGAGCTCAACTCCAGTATTG 3403  
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Qy 3404 AGGACCTTTCTGAAGCATCTATGCTTCAAGTGTATACAAAGTAATTTTAAAGTCAAGAG 3463  
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Db 3761 ATAATCAAAAGTGCAAAGAGAGATCGAAGCTGAAGAGAGAGGCTTTAGCGATCGCA 3820

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QY 3584 TGGCAATGTCAGCGTCTCAGGATGCCCTCCCCATAGTTCTCTAGCTGCGAGGTTGAAAATG 3643
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DB 3881 GAGNAGATATATCATCATATTATCAACAGGATACACAGAGACTCTCTCCAGGACATACCAAG 3940
QY 3704 CAATAACCGTATAGAGAGACACTGAATGGCTGAAAGTCAACAGATAGGCTTGGAG 3763
DB 3941 CGAAACAGCCTTACAGAGAGAGCGTGAATGGCTGAAAGCCAGAGATAGGCTCGGAG 4000
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DB 4001 CATTTCTTCTTGTATCAGCTCAAGATGTGGAACTGGAATTTAATGGCTGTAAAC 4060
QY 3824 AGTGACTTATGTCAGAAACACATCTTCTGAGCAAGAAAGTAGTAGAGCACTAAGAG 3883
DB 4061 AGTGACTTATGTCAGAAACACATCTTCTGAGCAAGAAAGTAGTAGAGCACTAAGAG 4120
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DB 4181 CGTGTGAGAGAGCAATTACAACTCTTCAATGATGATGGAGGGGATCGTGCTC 4240
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DB 4241 ACCTCTTGAGTAATATGAGCCCTTCAAGATCAGTAGTATTAACTACACTGAACAGT 4300
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DB 4301 TACTCCGTGGCTTCTGATCTCCATGAAACCAAAATCATTCACAGAGATGTCAAGGTG 4360
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QY 4184 CCAGTTGGCTCAAAAGAACTGTCGAGGAGAGTTTCCAGGACAAATTAAGTGGGCAAA 4243
DB 4421 CCAGTTGGCTCAAAAGAACTGTCGAGGAGAGTTTCCAGGACAAATTAAGTGGGCAAA 4480
QY 4244 TTGCATTTATGACACTGAGTACTAAGAGTCAACAGTATGAGAGAGCTGTATGTAT 4303
DB 4481 TTGCATTTATGACACTGAGTACTAAGAGTCAACAGTATGAGAGAGCTGTATGTAT 4540
QY 4304 GGAGTGTGGCTGTCTATTATAGAAATGGCTTGTGCAAAACCAACCATGGAATCGAGAA 4363
DB 4541 GGAGTGTGGCTGTCTATTATAGAAATGGCTTGTGCAAAACCAACCATGGAATCGAGAA 4600
QY 4364 AACACTCCAAATCATCTTGTGTTGATTTAAGATGCTAGTGCAACTACTCTCATCGA 4423
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QY 4660 AGCCAGTGGGAAACCTTACCTAAGTATGTGATTGACAAATCATGATCTGTACCTAAGC 4719
DB 4901 GGGCAGCGGGGAA-CGGTACCTAAGCATGTGATTGACAAATCATGACCTGTACCTAAGC 4959
QY 4720 TCAGTATGCA-AAAGCCCAAACTAGTCAGAAACTGTAAACTGTGCTTTCAAGAAGACTG 4778
DB 4960 TCGATATGACAGACATCTACAGCTCGTCAGGAAGTGCACACCCGCTTTACAGGACTG 5019
QY 4779 GCCCTAGTGAACAGGAAACCAATGAAGTTTGCATGACTAAATTCGAGAGACATAATTT 4838
DB 5020 GCTCTGGGGACCAAGGAGGCGATGGAGTTTGCATGACTAAAGACAGAGACATAATTT 5079
QY 4839 ATTTTGTGGAGCACTTTTTCAGCAA 4864
DB 5080 A--ATTTTGGAGCACTTTTTCAGCTA 5103

RESULT 14
AXX80912
ID AAX80912 standard; cDNA; 3911 BP.
XX
AC AAX80912;
XX
DT 03-NOV-1999 (first entry)
XX
DE Human MEK1 cDNA.
XX
KW Human MEK1 cDNA; Mitogen ERK Kinase Kinase 1 protein; MEK1; protease;
extracellular signal regulated kinase; ERK; signal transduction pathway;
regulation; apoptosis; protein kinase; cleavage; caspase; antibody;
kinase fragment; mutant MEK1 protein; NH2-terminal fragment; detection;
immunoreactive; diagnostic; therapeutic assay; reagent; disorder;
aberrant expression; activation; MEK1 gene product; DNA probe; primer;
selectively hybridise; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT
FT /tag= a
/product= "MEK1 protein"
/function= "Regulates cellular apoptosis"
mat_peptide 2052..3908
FT /tag= b
FT /note= "Active fragment that mediates apoptosis"
XX
PN WO9941385-A1.
XX
PD 19-AUG-1999.
XX
PF 12-FEB-1999; 99WO-US002974.
XX
PR 13-FEB-1998; 98US-00023130.
XX
PA (CADU-) CADUS PHARM CORP.
XX
PI Johnson GL;
XX
DR WPI; 1999-508649/42.
XX
P-PSDB; AAY26235.
XX
PT A new mammalian serine-threonine protein kinase for treating disorder
characterized by aberration of the enzyme gene.
XX
PS Claim 5a; Page 124-130; 149pp; English.
XX
CC The present sequence is an isolated human MEK1 cDNA. It encodes Mitogen
ERK Kinase Kinase 1 (MEK1) protein, which functions to integrate
proteases and signal transduction pathways involved in the regulation of
apoptosis. It is a 196 kDa protein kinase, which upon cleavage at Asp
681/684 by caspase generates a 91 kDa kinase fragment that induces
CC apoptosis and a 113 kDa NH2-terminal fragment. Mutant MEK1 proteins that
are resistant to cleavage by caspase proteases and capable of inhibiting
```

CC apoptosis can be produced. MEK1 proteins and antibodies immunoreactive  
CC with MEK1 proteins are used in diagnostic and therapeutic assays and  
CC reagents for detecting and treating disorders involving aberrant  
CC expression or activation of the MEK1 gene products. DNA probes or  
CC primers that selectively hybridise to MEK1 cDNA, can be used for its  
CC detection in samples  
XX  
SQ

Sequence 3911 BP; 1058 A; 973 C; 975 G; 905 T; 0 U; 0 Other;

Query Match 62.7%; Score 3286.4; DB 2; Length 3911;

Best Local Similarity 90.5%; Pred. No. 0;

Matches 3580; Conservative 0; Mismatches 331; Indels 45; Gaps 5;

590 CAGCCTCGAGGACGATGTTGGAAGGAGAAATAGCGAGGCCCTGTGGTGAATAC 649

1 CGGCTCGAAGCAGATGTTGGAAGGAGAAATAGCGAGGCCCTGTGGTGAATAC 60

650 CAATCCAGGTTAAAGGAGATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCCAGGAG 709

61 CAATCCAGGTTAAAGGAGATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCCAGGAG 120

710 AGGTCAGGAGGAGGCGGCTTCACAGCTTCCAAAGGCGCAGCAGTCTTCTCTGGCA 769

121 AGGTCAGGAGGAGGCGGCTTCACAGCTTCCAAAGGCGCAGCAGTCTTCTCTGGCA 180

770 ACTCCCATCAGGTCGACAGTGAATCAGAACTCTCCAGGAGTAAGGAGAAAGAGTTT 829

181 ACTCCCATCAGGTCGACAGTGAATCAGAACTCTCCAGGAGTAAGGAGAAAGAGTTT 240

830 CCCAGTGCCCTTTCAGAGTGGCAGAAATCACACCCCGGAGAGGCCCTTCCAGGATG 889

241 CCCAGTGCCCTTTCAGAGTGGCAGAAATCACACCCCGGAGAGGCCCTTCCAGGATG 300

890 GCTTCTCACATATAGCCCTCAGGAAACAAACCCCGTGTAAACAAAGTATGCGGGCCA 949

301 GCTTCTCACATATAGCCCTCAGGAAACAAACCCCGTGTAAACAAAGTATGCGGGCCA 360

950 GACTGTACTTACTGACAGATAGGGGCTAACTCTTCTGATGAGGAGAGAGGCCAG 1009

361 GACTGTACTTACTGACAGATAGGGGCTAACTCTTCTGATGAGGAGAGAGGCCAG 420

1010 ACAATAAATACCGGCTGTTATTTGGGCTCAGAACTGACAGTGTGACGTGGAACTTCT 1069

421 ACAATAAATACCGGCTGTTATTTGGGCTCAGAACTGACAGTGTGACGTGGAACTTCT 480

1070 GTATTCATCTGCTATTTGTGATGCTCCGGGTGTTTCAACTAGAACCTTCCAGCCCAATGT 1129

481 GTATTCATCTGCTATTTGTGATGCTCCGGGTGTTTCAACTAGAACCTTCCAGCCCAATGT 540

1130 TATGAGAAACCTTAAAGAAATTTGAGGTTGAGAGTTTGTCCGAAATATCACAGTA 1189

541 TATGAGAAACCTTAAAGAAATTTGAGGTTGAGAGTTTGTCCGAAATATCACAGTA 600

1190 GCGGTAGCTCAAGGATCAAGCTCCATCTCGTAACACCATCCAGAGTTTGTTCACGCA 1249

601 GCGGTAGCTCAAGGATCAAGCTCCATCTCGTAACACCATCCAGAGTTTGTTCACGCA 660

1250 TGTCAATTTCTCATATGTCATCATCTAGTACTTCTAGCTAGTTCAGAAACAGCA 1309

661 TGTCAATTTCTCATATGTCATCATCTAGTACTTCTAGCTAGTTCAGAAACAGCA 720

1310 TAAAGGATGAAGAGGAAACAGATGTCCTATTTGCTTGTGGGCGATGCTTGAAGAAA 1369

721 TAAAGGATGAAGAGGAAACAGATGTCCTATTTGCTTGTGGGCGATGCTTGAAGAAA 780

1370 GTCTTACAGTGTGTAAGACCGCTGCAGAAACAGCTGCACACCATGTCATGTCATTTT 1429

781 GTCTTACAGTGTGTAAGACCGCTGCAGAAACAGCTGCACACCATGTCATGTCATTTT 840

1430 GGGCAGAGAGTGTAGAGAAATAGAGAACTTTAATATGTCCTTGTAGATCTAAGT 1489

841 GGGCAGAGAGTGTAGAGAAATAGAGAACTTTAATATGTCCTTGTAGATCTAAGT 900

QY 1490 GGAGATCTCATGATTTCTACAGCCACGAGTTGTCAAGTCTCTGTGATTCCTCTTCCC 1549

DB 901 GGAGATCTCATGATTTCTACAGCCACGAGTTGTCAAGTCTCTGTGATTCCTCTTCCC 960

QY 1550 TCAGAGCTGTCACAGCAGCAAAACCGTACAGCAGCAGCCTTTGGCTGATCAAGAGGAATC 1609

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DB 1021 AAGAGAGCAATTTAACTTACTCATNTATGAACTCAGCAAAATCCTCTCTCTTACAAAG 1080

QY 1670 ATTTAGCTGAGCAGCAGTATTCAGGTTTGGAAATGGAATCGTTGGCTGCTTATTTCTA 1729

DB 1081 ATTTAGCTGAGCAGCAGTATTCAGGTTTGGAAATGGAATCGTTGGCTGCTTATTTCTA 1140

QY 1730 GAAACTGGAATGTGAGAGATGCGCTTCAGCGCTTCTTCCCATGATCTCAGTGGGGGCC 1789

DB 1141 GAAACTGGAATCGTAAGGGAATGCGCTTAGCGCTTCTTCCACAGCATCTAGTGGGGGCC 1200

QY 1790 TCTCTTGGCAATGGGAGAGCAGTGGAAATCTTGGGGGCGAGCAGTGGAGAGCCGCA 1849

DB 1201 TCTTGTGGCAATGGGAGAGCAGTGGAAATCTTGGAGGGCGAGTGGGGGAGCTTAA 1260

QY 1850 GTGGGGGAGCCACAGTGGGCTTCTCCAGACAGTATCTCAGGAGATGTGTGGAGCAT 1909

DB 1261 GCGCGGAGCGGCCAGCGGCTCTCCAGCCAGCATCTCAGGGGATGTGTGGAGCGT 1320

QY 1910 GCTGAGCGTTCTGTCAATGCTGTGTGCTGACCTCTTACAAAGTGTACGTTGTGCTT 1969

DB 1321 GCTGAGCGTCTGTCTATAGTCTGCGCTGACCTCTCTACAAAGTGTACGTTGTGCTT 1380

QY 1970 TAAACCAATTTGAGAGCCATGCTGTATATATCTCTTGTCCACAGTTTAGCGAAAGATCA 2029

DB 1381 TAAACCAATTTGAGAGCCATGCTGTATATATCTCTTGTCCACAGTCTGGCAGAAAGATCA 1440

QY 2030 AACTTCAGAGATCTTCCAGCCAGTGTAGACACCATCTTAGTCAAAATGTGAGAGTCCA 2089

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DB 1501 ACAGCGCAGCAGTGTGCTGTCTTCTACAGTGTGAACTGTGCAATGSCCAAGCAG 1560

QY 2150 GAGAGTGTGCTGCGAGAGAAATATCTAAAGCTGTGATTCATTTGTTTGTGTGTG 2209

DB 1561 GAAAGTGTGCTGCGAGAGAAATATCTAAAGCTGTGATTCATTTGTTTGTGTGTG 1620

QY 2210 ATTTGCTTAAATTTGATTTCTTGAACCAAACTGAATCAAACTTGGCAAGAACTTC 2269

DB 1621 ATTTGCTTAAATTTGATTTCTTGAACCAAACTGAATCAAACTTGGCAAGAACTTC 1680

QY 2270 TTGGCGCGCTTGTCTTATAGATAGCTGTGTGGAATTTCTGCTGAAATTTTATCTCTC 2329

DB 1681 TTGGCGCGCTTGTCTTATAGATAGCTGTGTGGAATTTCTGCTGAAATTTTATCTCTC 1740

QY 2330 ATATTTGCTAGTACTGATTTTCCAGAGCTGAGCCTGTTGAAATCAGGTATAGAGAGTGC 2389

DB 1741 ATATTTGCTAGTACTGATTTTCCAGAGCTGAGCCTGTTGAAATCAGGTATAGAGAGTGC 1800

QY 2390 TGTCTCTTAACTTTGCTTTGCACTCAATGATTAATTTCCACTCAATGTTGGCAAC 2449

DB 1801 TGTCTCTTAACTTTGCTTTGCACTCAATGATTAATTTCCACTCAATGTTGGCAAC 1860

QY 2450 TTTCCAGAGGATCTACTTGTGCTGAGAAATGTTTACTACAGTACCCATGTTT 2509

DB 1861 TCTCTCGAGGATATCTGAGCTCTGCCAGATGTTGAGCCAGTGTGCTGCTGTTT 1920

QY 2510 CAAAATGTTTGAATGCTGAGTGTTCAGTTCACCTTCCAGTTCACAGGATGCGTCCGC 2569

DB 1921 CCAAGCTGTGTAACCATGCTTAATGTTCTGCGCTCCACCATCTCAGGATGCGCCGC 1980

QY 2570 GTTTGATGCTATTGAGATGAGTGGAAATTTGCCGAGGCCATCCAGTGTGGCGTAGAG 2629

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Db 2041 ACACCTGTGGATGGGATCAGGACAG---CTTACAGGGGCTGGCCCCCGCCAGCTGTCT-- 2095  
QY 2690 AAACACAGAGAACAGTTCCTCCAGTGCACAGTCCATTTAGAGAACTGGAAAGGAT 2749  
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QY 2870 TGGTTCAAAACAAAGGACAGCCCAACAGTCAAGTGTGTAACCTCTCTCTCTTTATCTCATC 2929  
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Db 2716 CGGTGAGGACAAAGTGCAGGTTAGATGTGAACACGAGCTCACTCCAGCATTCAGGACC 2775  
QY 3410 TTCTTTGAAGCATCTATGCTTCAAGTGATACAAAGTAACATTTTAAGTCAGAGTGTCTG 3469  
Db 2776 TTCTTTGAAGCATCTATGCTTCAAGTGATACAAAGTAACATTTTAAGTCAGAGTGTCTG 2835  
QY 3470 TCCTGCTCTCTGAAAGGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3529  
Db 2836 TCCTCTCTCTCGGAAAGGCGGAAATGACACCTCAAGAGACAGCTCAATCATATC 2895  
QY 3530 AAAAGTGCAAAGAGAGATGGAAGCTGAAGAGAGAGAGCTTTTAGCAATTTGCCATGGCAA 3589  
Db 2896 AAAAGTGCAAAGAGAGATGGAAGCTGAAGAGAGAGAGCTTTTAGCAATTTGCCATGGCAA 2955  
QY 3590 TGTACAGCTCTCAGGATGCCCTCCCATAGTTCCTCAGCTGCGAGGTTGAAATGGAGAG 3649  
Db 2956 TGTACAGCTCTCAGGATGCCCTCCCATAGTTCCTCAGCTGCGAGGTTGAAATGGAGAG 3015  
QY 3650 ATATCATATTATTCAACAGGATACACAGAGACTCTTACCAGGATACACCAAGCAAAAC 3709

Db 3016 ATATTATCATCATTCAGCAGGACACACAGAAACTCTTCCAGGACATACCAAGGAAAC 3075  
QY 3710 AACCTATAGAGAGACACTGAATGGCTGAAGGTCAAACAGATAGCCTTCGAGCATTTT 3769  
Db 3076 AGCCTTACAGAGAGACGCTGAGTGGCTGAAGGCGCAGAGATAGGCTTCGAGCATTTT 3135  
QY 3770 CTTCTTGTATCAGGCTCAAGATGCGGAACTGGAACTTTAATGGCTCTTAAACAGAGTGA 3829  
Db 3136 CTTCTTGTATCAGGCTCAAGATGCGGAACTGGAACTTTAATGGCTCTTAAACAGAGTGA 3195  
QY 3830 CTTATGTCAGAAACAACATCTTCTGAGCAAGAGAGTAGTAGAGCACTATAGAGAGAGA 3889  
Db 3196 CTTATGTCAGAAACAACATCTTCTGAGCAAGAGAGTAGTAGAGCACTATAGAGAGAGA 3255  
QY 3890 TAAAGATGATGAGCCATCTGAATCATCCAAACATCATTTAGGATGTTGGAGCCAGCTGTG 3949  
Db 3256 TAAAGATGATGAGCCATCTGAATCATCCAAACATCATTTAGGATGTTGGAGCCAGCTGTG 3315  
QY 3950 AGAAGAGCAATTAACATCTCTTCAATGATGAGTGGAGGGGATCGGTGCTCATTTGC 4009  
Db 3316 AGAAGAGCAATTAACATCTCTTCAATGATGAGTGGAGGGGATCGGTGCTCATTTGC 3375  
QY 4010 TCAGTAAATATGAGCCCTTCAAGAACTCAGTAGTTATTAACTACACTCAACAGTTACTCC 4069  
Db 3376 TCGTAAATATGAGCCCTTCAAGAACTCAGTAGTTATTAACTACACTCAACAGTTACTCC 3435  
QY 4070 GTGGCTTTCTGATCTCCATGAAACCAAACTCATTCACAGAGATGCAAGGTGCAATTT 4129  
Db 3436 GTGGCTTTCTGATCTCCATGAGAACCAAGATCATTCACAGAGATGCAAGGTGCAATTT 3495  
QY 4130 TCGTAAATGAGCACTGCTCAGAGACTTAAGAAATGAGATTTTGGAGCTGCAGCCAGT 4189  
Db 3496 TCGTAAATGAGCACTGCTCAGAGACTTAAGAAATGAGATTTTGGAGCTGCAGCCAGT 3555  
QY 4190 TGGCATCAAAAGGAACTGGTCAGAGAGTTCAGGGAACAATTAAGTGGGGAACAATTCGAT 4249  
Db 3556 TGGCATCAAAAGGAACTGGTCAGAGAGTTCAGGGAACAATTAAGTGGGGAACAATTCGAT 3615  
QY 4250 TTATGGCACTCAGCTATCAGAGCTCAACAGTATGAGGAGGCTGTGATGTATGGAGTG 4309  
Db 3616 TCATGGCGCTCAGGTCCTAAGAGTCAAGAGTGTGGTAGGAGCTGTGATGTATGGAGTG 3675  
QY 4310 TTGGCTGTCTATTATAGAAATGGCTTGTGCAAAACCCACCATGGAAATCCAGAAAACACT 4369  
Db 3676 TTGGCTGTCTATTATAGAAATGGCTTGTGCAAAACCCACCATGGAAATCCAGAAAACACT 3735  
QY 4370 CCATCATCTCTGCTTGTATTTAAGATGCTAGTGCACACTACTCTCCATCGATCCCTTT 4429  
Db 3736 CCATCATCTCTGCTTGTATTTAAGATGCTAGTGCACACTACTCTCCATCGATCCCTTT 3795  
QY 4430 CACATTTGCTCTCTGCTTTACGAGATGCTGCTCTTTCGTTTGTAGAACTTCAACCTCAGG 4489  
Db 3796 CACACCTGTCCCTGGTTTACGAGATGCTGCTCTTTCGTTTGTAGAACTTCAACCTCAGG 3855  
QY 4490 ACAGCTCTCATCAGAGAGCTTACAGAGCATCCAGTCTTTCGTTTGTAGAACTTCAACCTCAGG 4545  
Db 3856 ACCGGCTCCGTCAAGAGAGCTGCTGAAACATCCCGTCTTCCTCGTACCACGCTGGTAG 3911

## RESULT 15

AAZ25069

ID AAZ25069 standard; cDNA; 3911 BP.

XX

AC AAZ25069;

XX

DT 09-DEC-1999 (first entry)

XX

DE Human MEK1 nucleotide sequence.

XX

KW MEK1; MEK2; MEK3; mitogen-activated protein kinase; MAPK; ERK;

KW extracellular regulated kinase; signal transduction; regulation;

KW MAPK/ERK; MEK; MEK3; inflammation; cellular proliferation;

KW differentiation; development; cell death; ss.

XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 3..3911  
FT /\*tag= a  
FT /product= "MEKK1"  
XX PN WO9947686-A2.  
XX PD 23-SEP-1999.  
XX PF 15-MAR-1999; 99WO-US005556.  
XX PR 16-MAR-1998; 98US-0078153P.  
XX PR 04-SEP-1998; 98US-0099165P.  
XX PA (CADU-) CADUS PHARM CORP.  
XX PI Johnson GL;  
XX WPI; 1999-571843/48.  
XX DR P-PSDB; AAY42104.  
XX PT New human MEKK polynucleotides and polypeptides, used for regulating  
XX PT signal transduction in cells.  
XX PS Claim 2; Fig 1; 159pp; English.  
XX CC The present sequence encodes human mitogen-activated protein kinase/  
XX CC extracellular response kinase (MAPK/ERK) kinase kinase (MEKK),  
XX CC specifically designated MEKK1. The MEKK proteins are used to modulate and  
XX CC regulate signal transduction in cells, as well as for regulation of gene  
XX CC transcription in a cell encoding MEKK, where the cell is involved in  
XX CC inflammation, regulation of cellular proliferation and differentiation,  
XX CC regulation of development, regulation of cell death or regulation of  
XX CC inflammation. They are also used to prepare antibodies. MEKK  
XX CC polynucleotides can be used to produce the protein recombinantly and as a  
XX CC source of probes and primers  
XX SQ Sequence 3911 BP; 1058 A; 973 C; 975 G; 905 T; 0 U; 0 Other;

Query Match 62.7%; Score 3286.4; DB 2; Length 3911;  
Best Local Similarity 90.5%; Pred. No. 0;  
Matches 3580; Conservative 0; Mismatches 331; Indels 45; Gaps 5;

QY 590 CAGCCTGGAAGCACCAATGGTTGGAAAGGAGAAATAGCGAGGCGCTGTGTGTAAAC 649  
DB 1 CGGCTGGAAGCACAGTGGTTGGAAAGGAGAAATAGCGAGGCGCTGTGTGTAAAC 60  
QY 650 CAATCCAGTTAAAGGAGATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCAGGAG 709  
DB 61 CAATCCAGTTAAAGGAGATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCAGGAG 120  
QY 710 AGGTCCAGGCAAGTCGGCTTACCAGCTTCCAAAGGCGGAGCGAGTCTTCTCTGCA 769  
DB 121 AGGTCCAGGCAAGTCGGCTTACCAGCTTCCAAAGGCGGAGCGAGTCTTCTCTGCA 180  
QY 770 ACTCCCTCATGGTCCGACAGTGAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAAT 829  
DB 181 ACTCCCTCATGGTCCGACAGTGAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAAT 240  
QY 830 CCCAGTCCCTTTCAGAGTGCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAAT 889  
DB 241 CCCAGTCCCTTTCAGAGTGCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAAT 300  
QY 890 GCTTCTCACCATTATAGCCCTCAGGAAACAAACCGCGCTGTTAAACAAAGTGTAGGGGCA 949  
DB 301 GCTTCTCACCATTATAGCCCTCAGGAAACAAACCGCGCTGTTAAACAAAGTGTAGGGGCA 360  
QY 950 GACTGTACTTACTGAGCGAGTAGGGCTTACTTCTGATTTGGAGGAGACAGCCGAG 1009  
DB 361 GACTGTACTTACTGAGCGAGTAGGGCTTACTTCTGATTTGGAGGAGACAGCCGAG 420

QY 1010 ACAATAAATACCGGGTGTATTATGGCCCTCAGAACTGCAGCTGTGCACGTGGAACATTCT 1069  
DB 421 ACAATAAATACCGGGTGTATTATGGCCCTCAGAACTGCAGCTGTGCACGTGGAACATTCT 480  
QY 1070 GTATTCAATCTGCTATTATTGTGATGCTCCGGGTGTTCCTCACTAGAACTTCCAGACCCATGT 1129  
DB 481 GTATTCAATCTGCTATTATTGTGATGCTCCGGGTGTTCCTCACTAGAACTTCCAGACCCATGT 540  
QY 1130 TATGGAGAAAACTTTAAAGAAATTTAGGTTGAGAGTTTGTTCAGAAATATCAGATTA 1189  
DB 541 TATGGAGAAAACTTTAAAGAAATTTAGGTTGAGAGTTTGTTCAGAAATATCAGATTA 600  
QY 1190 GCGTAGCTCAAGGATCAAGCTCCATCTCGTAAACCAATCCAGAAATTTGTTCACGCA 1249  
DB 601 GCGTAGCTCAAGGATCAAGCTCCATCTCGTAAACCAATCCAGAAATTTGTTCACGCA 660  
QY 1250 TGTCAAAATCTCATACATTGTCTATCTAGTACTTCTACGTCTAGTTCAGAAAAACAGCA 1309  
DB 661 TGTCAAAATCTCATACATTGTCTATCTAGTACTTCTACGTCTAGTTCAGAAAAACAGCA 720  
QY 1310 TAAAGGATGAAGGAAACAGATGTGTCTATTGTGTGTGGCATGCTTGTATGAAGAAA 1369  
DB 721 TAAAGGATGAAGGAAACAGATGTGTCTATTGTGTGTGGCATGCTTGTATGAAGAAA 780  
QY 1370 GTCTTACAGTGTGTGAAGACGCTGCAGGAAACAGCTGCACCACTCATGTCAATTT 1429  
DB 781 GTCTTACAGTGTGTGAAGACGCTGCAGGAAACAGCTGCACCACTCATGTCAATTT 840  
QY 1430 GGCAGAGAGTGTGAAGAAATAGAGAACTTTAATATGTCCCTTTGTAGATCAAGT 1489  
DB 841 GGCAGAGAGTGTGAAGAAATAGAGAACTTTAATATGTCCCTTTGTAGATCAAGT 900  
QY 1490 GAGATCTCATGATTTCTACGCCAGAGTGTCTGAAGTCTCTGAGATCCCTTCTTCCC 1549  
DB 901 GAGATCTCATGATTTCTACGCCAGAGTGTCTGAAGTCTCTGAGATCCCTTCTTCCC 960  
QY 1550 TCAGAGCTGCACAGCAGCAAAACCGTACAGCAGCAGCTTTGGCTGATCAGAAAGAAATC 1609  
DB 961 TCAGAGCTGCACAGCAGCAAAACCGTACAGCAGCAGCTTTGGCTGATCAGAAAGAAATC 1020  
QY 1610 AAGAGAGCAATTTTAACCTTACTCATTATGGAACTCAGCAAAATCCCTCTCTTCAAG 1669  
DB 1021 AAGAGAGCAATTTTAACCTTACTCATTATGGAACTCAGCAAAATCCCTCTCTTCAAG 1080  
QY 1670 ATTATAGCTGAGCATGGATTCAGGTTTGGAAATGGAATCGTTGGCTCTTATTCTTA 1729  
DB 1081 ATTATAGCTGAGCATGGATTCAGGTTTGGAAATGGAATCGTTGGCTCTTATTCTTA 1140  
QY 1730 GAAACTGGAAATGTGAGAGATGGCCCTCAGCGTCTTCCCATGATGTAGTGGGGCCC 1789  
DB 1141 GAAACTGGAAATGTGAGAGATGGCCCTCAGCGTCTTCCCATGATGTAGTGGGGCCC 1200  
QY 1790 TGCTGTGGCAATGGGAGAGCAGCTGGAAATTTCTGGGGGAGCAGTGGAAAGCAGCCCCA 1849  
DB 1201 TGCTGTGGCAATGGGAGAGCAGCTGGAAATTTCTGGGGGAGCAGTGGAAAGCAGCCCCA 1260  
QY 1850 GTGGGGAGCCACAGTGGGTCTTCCAGAACAGTATCTCAGAGAGATGTGTGGAGGAT 1909  
DB 1261 GCGCGGAGCGGCGAGCGGCTCTCCAGCCAGCATCTCAGGGGATGTGTGGAGGCGT 1320  
QY 1910 GCTGACAGCTTCTCAATGGTCTGTGCTGACCCCTGTCTACAAAGTGTAGTGTGCTT 1969  
DB 1321 GCTGACAGCTTCTCAATGGTCTGTGCTGACCCCTGTCTACAAAGTGTAGTGTGCTT 1380  
QY 1970 TAAAAACATTGAGAGCCATGCTGGTATATATCTCTTGGCACAGTTTAGCGGAAGAAATCA 2029  
DB 1381 TAAAAACATTGAGAGCCATGCTGGTATATATCTCTTGGCACAGTCTGGCAGAAAGAAATCA 1440  
QY 2030 AACTTCAGAGATCTTCCAGCCAGTGTGTAGACCACTCTCTTCCAGAGTCTGGCAGAGTCCCA 2089  
DB 1441 AACTTCAGAGATCTTCCAGCCAGTGTGTAGACCACTCTCTTCCAGAGTCTGGCAGAGTCCCA 1500

QY 2090 ATAGCGCACAAGTCAGCTGCTCCATATCAACACTGTTGGAACTGTGCAGAGGCCAAGCAG 2149  
DB 1501 ACAGCGCACAGTCAGCTGCTCCATATCTACAGTCTGGAATCTGCAATGGCCCAAGCAG 1560  
QY 2150 GAGAGCTTGGCAGTGGCAGAGAAATCTAAAAGCTGGATCCATGGTATTGGTGTGTTG 2209  
DB 1561 GAAAGCTGGCGTGGGAGAGAAATCTAAAAGCTGGTCCATCGGGTGGTGTGTCG 1620  
QY 2210 ATTATGCTTAAATGTTATCTTGGAAACCAAACTGAATCAAACTGAAGCAAACTTC 2269  
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QY 2270 TTGGCGGCTTTGCTCTATAGACTGTTGTTGGAAATTTCCCTGCTGAATTTTATCCTC 2329  
DB 1681 TGGGTGCGCTCTGCTCTATAGACTGTTGTTGGAAATTTCCCTGCTGAATTTTATCCTC 1740  
QY 2330 ATATTGTCAGTACTGATGTTTCAAGCTGAGCTGTTGAAATGAAATGAAATGAAATGAA 2389  
DB 1741 ATATTGTCAGTACTGATGTTTCAAGCTGAGCTGTTGAAATGAAATGAAATGAAATGAA 1800  
QY 2390 TGTCCCTCTTAACCTTTGCTTTGCACTGCTATGATTAATCCCACTCAATGGTTGCGCAAC 2449  
DB 1801 TCTCCCTCTTAACCTTTGCTTTGCACTGCTATGATTAATCCCACTCAATGGTTGCGCAAC 1860  
QY 2450 TTTCCAGAGGATCTACTGAGTTCTGCAAGAAATGGTTACTACAGTACCCCATGTTT 2509  
DB 1861 TCTCTCGGAGGATATCTGAGCTCTGCCAGATGGTGACCGAGTGCCTGCTGTTT 1920  
QY 2510 CAARACTGTTGAATGCTGAGTGTTCAGTTCACCTTCACCTTCACAGGATGGTCCGC 2569  
DB 1921 CCAAGCTGTTAACCATGCTTAATGCTTCTGCTCCACCCACTTACCAGGATGGCGCGC 1980  
QY 2570 GTTTGATGCTATTGTCAGATGAGTGGAAATGGCGAGGATCCAGTTGGGCGCTAGAAG 2629  
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DB 2041 ACACCTTGGATGCTCAACAGGACAGCTTCTGCGAGGATCTGTTCCCACTATCTGG - 2095  
QY 2690 AAACACAGAGAACTGCTTCCCTGAGTGCACAGTCCATTTAGAGAAACTGGAAGGAT 2749  
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QY 2810 CAGTAGGACCTTCTAGTTCAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2869  
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QY 2870 TGGTTCAACAAAGGAGAGACCCACAGTCAAGTGTGTTGAACTCCCTCTCTTTATCTCATC 2929  
DB 2254 CGGTTCAACAAAGGAGAGACCCACAGTCAAGTGTGTTGAACTCCCTCTCTTTATCTCTC 2310  
QY 2930 ATTCCCAATTAATGTTCCAGCTTGTCAACCCCTTCTTCTTACCCCTCTGTTACCCAG 2989  
DB 2311 ATGCTCAATTAATGTTCCAGCACCATCAGCCCTTGTCTCTGCGCCGCTCTGTC--- 2367  
QY 2990 CTGGCACTGCAACAGATGCTCTTAAGCATGAGTCTCAGGATTCATTCCTCTGCAATAC 3049  
DB 2368 -----CAGATATTTCTAAGCAGACAGCCCGGCAATTTGTTCCCTCTGCAAAATAC 2415  
QY 3050 CTTCTGCATCTCTCAACACAGCGCAAGTGTCTCTCAATTTCCACAGAACTGTCCTG 3109  
DB 2416 CTTCTGCATCTCTCAACACAGCGCAAGTGTCTCTCAATTTCCAGAGAACTGTCCTG 2475  
QY 3110 AAAACAAAGACTCAGATAAATTTCCCGAGCTTTTACTCAGTCAAGACCTTGGCCCTCCA 3169  
DB 2476 AACACGAGACTCAGACAGCTCTCCCGAGCTTCTCACTCAGTCAAGACCCCACTCCA 2535  
QY 3170 GTAACATACAGGCGCAAGGCTCTAGACCTTACCCAGGTAATACAGTAAACAGGAG 3229

DB 2536 GTAACATACAGGCGCAAGGCTCTAGACCTCCGACCGCTTCCGGGAGTACAGCAAACTAGGG 2595  
QY 3230 ATCCCTCTCAAAAATAGCATGACACTTGTATCTGAAACAGTAGTTCCAAAATGTATGACAGCT 3289  
DB 2596 ACGCCACAAAATAGTACCATGACACTTGTATCTGGGAGTGTCTTCCAGGTGTGACAGAGCT 2655  
QY 3290 TTGGCTGTAGAGCAATAGTAGTAAATGCTGTATATCCAGTGTACCCAGTGTACAGAGCTTCA 3349  
DB 2656 TTGGCGGCGCGCAACAGTGGCAACGCGCTCATACCCAGGACAGAGACAGTGTTCAGCG 2715  
QY 3350 CAGTAGAGAGAAATGTCAGATGTAGATGTCAATACAGAGCTCAATCCAGTATTAGAGGACC 3409  
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QY 3410 TTTCTGAAGCATCTATGCTTCAAGTGTCAAGTGTAACTTTTAAGTCAAGAGTGTCTG 3469  
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DB 2836 TCTCTCTCTCGGAAAGGCGGAAATGACACACCTTCAAGAGCAGCTCAATCATATC 2895  
QY 3530 AAAAGTCAAAAGAGAGATGGAAGCTGAAGAGAAAGAGCTTTAGCAATTTGCCATGGCA 3589  
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DB 2956 TGTGAGCTCTCAGAGTGCCTCCCATAGTTCTCAGCTGAGCTGAAATGGAGAG 3015  
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DB 3016 ATATTCATCTATTCAGCAGGACACACAGAGAACTCTTCCAGGACATACCAAGCAAAAC 3075  
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QY 3770 CTTCTTGTATTAGGCTCAAGATGTGGGAACTGGAACCTTTAATGCTGTTTAAACAGGTA 3829  
DB 3136 CTTCTTGTATTAGGCTCAAGATGTGGGAACTGGAACCTTTAATGCTGTTTAAACAGGTA 3195  
QY 3830 CTTTATGTCAGAACACATCTTCTGAGCAGAGAGAGTGTAGAACACATTAACAGAGAGAG 3889  
DB 3196 CTTTATGTCAGAACACATCTTCTGAGCAGAGAGAGTGTAGAACACATTAACAGAGAGAG 3255  
QY 3890 TAAAGATGATGAGCCATCTGAATCTCAAAACATCATTTAGGATGTTGGAGGCCAGCTGTG 3949  
DB 3256 TAAAGATGATGAGCCATCTGAATCTCAAAACATCATTTAGGATGTTGGAGGCCAGCTGTG 3315  
QY 3950 AGAGAGCAATTAACATCTTCTTATGATGATGAGGAGGAGTGGGCTGCTATTCG 4009  
DB 3316 AGAGAGCAATTAACATCTTCTTATGATGATGAGGAGGAGTGGGCTGCTATTCG 3375  
QY 4010 TGAATTAATGATGAGGCTTCAAAAGATCAGTAGTTATTAACTTACACTGAACTAGTTACTCC 4069  
DB 3376 TGAATTAATGATGAGGCTTCAAAAGATCAGTAGTTATTAACTTACACTGAACTAGTTACTCC 3435  
QY 4070 GTGGCTTTCTGATCTCTCATGAAACCAATCATTTACAGAGATGTCAAGGTGCCAAT 4129  
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QY 4130 TGTAAATGACAGCACTGGTCAAGAGTAAAGAAATTTGAGATTTTGGAGCTGCAGGCCAGGT 4189  
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DB 3556 TGGCATCAAAAGGAACTGGTGCAGGAGTGTTCAGGCAAAATTACTGGGGCAATTTGCT 3615  
QY 4250 TTTATGCACTGAGTGTACTTAAGAGGTCAACAGTATGAAAGGAGCTGTGATGTATGGAGTG 4309



Db 3616 TCATGGCGCCTGAGTCTCTAAGAGGTCAGCAGTATGGTAGAGCTGTGATGTATGGAGTG 3675  
Qy 4310 TTGCTGTGCTATTATAGAAATGGCTTGTGCAAAACCAACCATGGAATGCAGAAAAACACT 4369  
Db 3676 TTGCTGCGCCATTATAGAAATGGCTTGTGCAAAACCAACCTTGGAAATGCAGAAAAACACT 3735  
Qy 4370 CCAATCATCTTGCTTTTGATATTTAAGATTGCTAGTGCAACTACTGCTCCATCGATCCCTT 4429  
Db 3736 CCAATCATCTGCGCTTGATATTTAAGATTGCTAGCGCAACTACTGCACCGTCCATCCCGT 3795  
Qy 4430 CACATTTGCTCCTGGTTTACGAGATGGGCTCTTGGTTGTTAGAACTTCAACCTCAGG 4489  
Db 3796 CACACCTGTCCCTGGTTTACGAGATGGGCTCTTGGTTGTTAGAACTTCAACCTCAGG 3855  
Qy 4490 ACAGACCTCCATCAAGAGAGCTACTGAAGATCCAGTCTTTCGTACTACATGGTAG 4545  
Db 3856 ACCGGCCTCCGTCAGAGAGCTGCTGAACATCCGGTCTCCGTACACCGTGGTAG 3911

Search completed: May 14, 2004, 15:07:58  
Job time : 1824 secs